

GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 25, 2003, 12:44:54 ; Search time 1420 Seconds

(without alignments)  
1129.122 Million cell updates/sec

Title: US-09-801-115B-2

Perfect score: 508

Sequence: 1 MDVQPKIKHAPFCFSYKGH.....LFNSGPYQKKPKVHEKKEVL 99

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODU=frame+2n.model -DEV=xlp  
-O=/gen2.1/SPFO\_spool/US09801115/unat\_20062003.141103\_13596/app.query.fasta.1.263  
-DB-EST -QFMT=fastap -SUFFIX=first -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR.SCORE=Pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=fto -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09801115.ecgn.1.1.2874.gunat.20062003.141103.13596 -MCPU=6 -ICPU=3  
-NO\_MAP -LARGEDEV -NEG.SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-FEAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1:	em_estba:*
2:	em_esthum:*
3:	em_estlin:*
4:	em_estlmu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_hic:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_hic:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estom:*
17:	gb_gss:*
18:	em_gss_hum:*
19:	em_gss_inv:*
20:	em_gss_pln:*
21:	em_gss_vrt:*
22:	em_gss_fun:*
23:	em_gss_mam:*
24:	em_gss_mus:*
25:	em_gss_other:*
26:	em_gss_pro:*
27:	em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	100.0	386	AA911088	AA911088 OK67E01.s
2	508	100.0	391	AI989739	AI989739 wu2le10.x
3	508	100.0	396	AW183193	AW183193 xj67f11.x
4	508	100.0	399	AA516431	AA516431 ne58a03.s
5	508	100.0	402	AI989747	AI989747 wu2le109.x
6	508	100.0	404	BMS53678	BMS53678 AGENCOURT
7	508	100.0	409	AI826623	AI826623 w35d10.x
8	508	100.0	423	AI128804	AI128804 q94d08.s
9	508	100.0	432	AA455042	AA455042 aa04a07.s
10	508	100.0	432	AA429945	AA429945 zw67f10.s
11	508	100.0	452	AI078580	AI078580 cz37h05.x
12	508	100.0	453	AI743235	AI743235 w99a002.x
13	508	100.0	468	BF109912	BF109912 717f103.x
14	508	100.0	510	BF399486	BF399486 UT-R-CA1
15	508	100.0	524	BG705303	BG705303 602687808
16	508	100.0	534	BG031757	BG031757 602299819
17	505	99.4	487	BM472086	BM472086 AGENCOURT
18	504	99.2	386	AA989129	AA989129 or75h10.s
19	504	99.2	781	BG529072	BG529072 602579169
20	504	99.2	962	BG249994	BG249994 60262062
21	491	96.7	529	BF691818	BF691818 602247787
22	484	95.3	443	BG613984	BG613984 602641513
23	480	94.5	432	AV759888	AV759888 AV759888
24	476.5	93.8	395	AI141284	AI141284 q852h10.s
25	475	93.5	353	AI265924	AI265924 qx68a08.x
26	475	93.5	930	BF203359	BF203359 601865968
27	472	92.9	468	W52820	W52820 zc35c06.tl
28	471.5	92.8	527	AA876539	AA876539 oa48h08.s
29	471.5	92.8	534	BO130559	BO130559 i18a06.x
30	471.5	92.8	534	BO613826	BO613826 i116a04.x
31	471.5	92.8	551	AA702011	AA702011 z17f0d02.s
32	471.5	92.8	551	AF151058	AF151058 Homo sapi
33	471.5	92.8	776	AV683453	AV683453 AV683453
34	471.5	92.7	409	N89912	N89912 zb22g09.s1
35	467.5	92.0	789	BE737159	BE737159 601305091
36	465.5	91.6	542	BO129993	BO129993 i148h06.x
37	463	91.1	543	BG532587	BG532587 602562152
38	460.5	90.6	678	B1561562	B1561562 603256264
39	452	89.0	333	AA987264	AA987264 os11a06.s
40	445.5	87.7	500	AI633679	AI633679 tnl1c04.x
41	445.5	87.7	654	BF791773	BF791773 602251973
42	444	87.4	326	AI263261	AI263261 qp62b12.x
43	442.5	87.1	606	W93646	W93646 zd97d08.s1
44	436	85.8	456	BE875161	BE875161 601488641
45	435	85.6	319	AI349474	AI349474 qp72f07.x

## ALIGNMENTS

RESULT 1	AA911088/c	AA911088	386 bp	MRNA	linear	EST 09-JUN-1998
LOCUS	OK67E01.s1	NCI_CGAP_G44	Homo sapiens	cDNA	clone IMAGE:1519032 3'	
DEFINITION	RNA sequence.					
ACCESSION	AA911088					
VERSION	AA911088.1	GI:3050378				
KEYWORDS	EST.					
ORGANISM	human.					
SOURCE	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.					
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.					
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),					



IMAGE:2662317 3', mRNA sequence.  
 ACCESSION AM183193  
 VERSION AM183193.1 GI:6451679  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 396)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 TITLE Unpublished (1997)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: [cgapsb-remail.nih.gov](mailto:cgapsb-remail.nih.gov)  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Seq primer: -40up from Glibco.  
 FEATURES  
 location/Qualifiers  
 1..396  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2662317"  
 /clone.lib="Soares\_NFL\_T\_GBC\_S1"  
 /lab\_host="DH10B"  
 /note="Organ: pooled. Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site\_1: Not I; Site\_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NH7, and B-cell NCI-CGAP GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 115 a 92 c 80 g 109 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 4,24e-59 Length: 396  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0  
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 QY 1 MetaspasnValGlnProlysilLeysHisArgProPhecysPheSerVallysglyHis 20  
 DB 359 ATGGATTAACGTCAGCGCAAAATTAACATCGCCCTTGTGCTTGAAGTGAAGCCAC 300  
 QY 21 VallysmetLeuArgleuAspIleleasnsrLeuValThrThValPheMetLeuile 40  
 DB 299 GTGAAGATGCTCGCGGTGATATTAACATCAGTGTGAACAAGATATTCATGCTCATC 240  
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThLeuThValIglyIglyValPhe 60  
 DB 239 GTATCTGTGTGGCACTGATACCAAGAACATTCAGATTGCTGTGAGGCGTGT 180  
 QY 61 AlaLeuValThrAlaValIcysCysLeuAlaAspGlyAlaLeuIleTyArgIysLeu 80  
 DB 179 GCACCTGTGACAGCAATATGCTGTGCGGAGGCGCCCTTATTTACCGGAAGCTTTCG 120  
 QY PheasnProSerGlyProTyrgInlyslsProValHIsGluIysGluValleu 99  
 DB 119 TTCATCCCAAGCGGCTCTTACCAAGAAAAGCTGTGCAAGAAAAGAAAGTTTGG 63  
 RESULT 4  
 AA516431/c  
 LOCUS AA516431 399 bp mRNA linear EST 13-AUG-1997

ne58a03.s1 NCI-CGAP\_C03 Homo sapiens CDNA clone IMAGE:901516 3', mRNA sequence.  
 ACCESSION AA516431  
 VERSION AA516431.1 GI:2255955  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 399)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 TITLE Unpublished (1997)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: [cgapsb-remail.nih.gov](mailto:cgapsb-remail.nih.gov)  
 Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arraying: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: [www-bio.llnl.gov/bdrp/image/image.html](http://www-bio.llnl.gov/bdrp/image/image.html)  
 Insert length: 527 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham.  
 FEATURES  
 location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:901516"  
 /clone.lib="NCI-CGAP\_C03"  
 /sex="pooled"  
 /tissue\_type="colon"  
 /lab\_host="DH10B"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization."  
 BASE COUNT 115 a 94 c 81 g 109 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 4,28e-59 Length: 399  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-801-115B-2 (1-99) x AA516431 (1-399)  
 QY 1 MetaspasnValGlnProlysilLeysHisArgProPhecysPheSerVallysglyHis 20  
 DB 357 ATGGATTAACGTCAGCGCAAAATTAACATCGCCCTTGTGCTTGAAGTGAAGCCAC 298  
 QY 21 VallysmetLeuArgleuAspIleleasnsrLeuValThrThValPheMetLeuile 40  
 DB 297 GTGAAGATGCTCGCGGTGATATTAACATCAGTGTGAACAAGATATTCATGCTCATC 238  
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThLeuThValIglyIglyValPhe 60  
 DB 237 GTATCTGTGTGGCACTGATACCAAGAACATTCAGATTGCTGTGAGGCGTGT 178  
 QY 61 AlaLeuValThrAlaValIcysCysLeuAlaAspGlyAlaLeuIleTyArgIysLeu 80  
 DB 177 GCACCTGTGACAGCAATATGCTGTGCGGAGGCGCCCTTATTTACCGGAAGCTTTCG 118  
 QY PheasnProSerGlyProTyrgInlyslsProValHIsGluIysGluValleu 99

Db 117 TTCATCCAGCGGCTTACCAAGAAAAGCTGTGATGAAAGAAAGTTTG 61

RESULT 5  
AI989747/c 402 bp mRNA linear EST 27-OCT-1999  
LOCUS AI989747  
DEFINITION WU21F09.x1 Soares-Dieckgraefe.colon\_NHCD Homo sapiens cDNA clone  
IMAGE:2520713 3', mRNA sequence.

ACCESSION AI989747  
VERSION AI989747  
KEYWORDS GI:5836628  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
1 (bases 1 to 402)  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: 40UP from Gibco.

FEATURES  
source  
1..402  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2520713"  
/clone\_lib="Soares-Dieckgraefe.colon\_NHCD"  
/tissue\_type="colonic mucosa from 3 patients with Crohn's  
disease"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTACCACTCTGAAGTGGAGCGCGCCGCTCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization. Tissue samples  
provided by Dr. Brian Dieckgraefe (Washington University,  
dieck@u.wustl.edu); colonic mucosa represents a range of  
disease involvement from moderate to severe Crohn's  
disease; samples include both perforating (fistulas) and  
non-perforating samples. Library constructed by Bento  
Soares and M. Fatima Bonaldo.

BASE COUNT 113 a 82 g 117 t  
ORIGIN

Alignment Scores:  
Pred. No.: 4,33e-59 Length: 402  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-801-115b-2 (1-99) x AI989747 (1-402)

QY 1 MetaspasvAlGlnProLySIlleLySHISArgProPhEcYsPhSeSerValLySGLyHIS 20  
Db 368 ATGGATTAACGTGCGACGCCGAAATATAACATCGCCCTTCTGCTTCACTGTGAAGGCCAC 309

QY 21 ValLySMetLeuArgLeuAspLlelleAsnSerLeuValThrThrValPheMetLeuIle 40  
Db 308 GTGAAGATGCTGGCGGTGATATATATACCTGATACACAGATTCATCTCATC 249

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
Db 248 GTATCTGTGTGGCACTGATACCAAGAACACACATTGACAGTTGTGTGAGGGGTGTTT 189

QY 61 AlaleuValThrAlaValCysCysLeuAlaAspGlyValaleuIleTyraGlyLeuIleu 80  
Db 188 GCACCTTGACAGACAGATATGCTGCTTCCGACGCGGCCCTTATTATACCGAAGCTTCTG 129

QY 81 PheAsnProSerGlyProTyrgLInLySLeuProValHisGluSylsGluValLeu 99  
Db 128 TTCATCCAGCGGCTTACCAAGAAAAGCTGTGATGAAAGAAAGTTTG 72

RESULT 6  
BM553628 404 bp mRNA linear EST 20-FEB-2002  
LOCUS BM553628  
DEFINITION AGENCOURT 6541772 NIH\_MGC\_88 Homo sapiens cDNA clone IMAGE:5740478  
5', mRNA sequence.  
ACCESSION BM553628  
VERSION BM553628  
KEYWORDS GI:18792524  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.  
1 (bases 1 to 404)  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: ARCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM2755 row: h column: 15  
High quality sequence stop: 403.

FEATURES  
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Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5740478"  
/clone\_lib="NIH\_MGC\_88"  
/tissue\_type="duodenal adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: small intestine; Vector: pCMV-SPORT6;  
Site:1: NotI; Site:2: SalI; Cloned unidirectionally;  
oligo-dT primed. Average insert size 1.767 kb. library  
enriched for full-length clones and constructed by Life  
Technologies. Note: this is a NIH\_MGC library."

BASE COUNT 121 a 80 c 116 t  
ORIGIN

Alignment Scores:  
Pred. No.: 4,36e-59 Length: 404  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-801-115b-2 (1-99) x BM553628 (1-404)

QY 1 MetaspasvAlGlnProLySIlleLySHISArgProPhEcYsPhSeSerValLySGLyHIS 20  
Db 32 ATGGATTAACGTGCGACGCCGAAATATAACATCGCCCTTCTGCTTCACTGTGAAGGCCAC 91

QY 21 ValLySMetLeuArgLeuAspLlelleAsnSerLeuValThrThrValPheMetLeuIle 40  
Db 92 GTGAAGATGCTGGCGGTGATATATATACCTGATACACAGATTCATCTCATC 151

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
Db 152 GTATCTGTGTGGCACTGATACCAAGAACACACATTGACAGTTGTGTGAGGGGTGTTT 211



QY 61 AlaleuValThralaValCysCysLeuAlaAspGlyAlaLeuIleTyraTglsLeu 80  
 Db 212 GCATTGTGACAGAGATGCTGCTGCGACGGGGCCCTTTATTCGGAAGCTTCTG 271  
 QY 81 PheasnProserGlyProTyrglnLysLysProValHisGluLysGluValLeu 99  
 Db 272 TTCATCCAGCGGCTCTTACAGAAAAGCCCTGTGATGAAAAAAGAAAGTTTTC 328

RESULT 7  
 LOCUS A1826623 409 bp mRNA linear EST 21-DEC-1999  
 DEFINITION W35d10.x1 NCI\_CGAP\_Pt22 Homo sapiens CDNA clone IMAGE:2417395 3',  
 mRNA sequence.  
 ACCESSION A1826623  
 VERSION A1826623.1 GI:5447294  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 409)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www.bio.lnln.gov/bhrp/image/image.html  
 Insert length: 462 Std Error: 0.00  
 Seq primer: -400p from Gldco.  
 Location/Qualifiers  
 source 1..409  
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 /db\_xref="taxon:9606"  
 /clone\_image="2417395"  
 /clone\_lib="NCI\_CGAP\_Pt22"  
 /sex="male"  
 /tissue\_type="normal prostate"  
 /lab\_host="DH10B"  
 /note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)  
 with a modified polylinker; 1st strand cDNA was prepared  
 from normal prostate bulk tissue, and was then primed with  
 a Not I - oligo(dT) primer. Double-stranded cDNA was  
 ligated to Eco RI adaptors (Pharmacia), digested with Not  
 I and cloned into the Not I and Eco RI sites of the  
 modified pT73 vector. Library is normalized, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 112 a 94 c 80 g 123 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.44e-59 Length: 409  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x A1826623 (1-409)

QY 1 MetaspasnaValGlnProLysIleLysHisArgProPhcCysPheSerValLysGlyHis 20  
 Db 367 ATGGATTACGTCGACGCGAATAAATCATGCCCCCTTCTGCTCAGGTGAAGGCGCAC 308  
 QY 21 VallysketLeuAglLeuAspIlelleLeuSerLeuValThrThrValPheMetLeuIle 40

Db 307 GTGAAGATGCTGCGGCTGGATATTAACACTGCTGTAACAGATATTCATCTCATC 248  
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
 Db 247 GTATCTGTGTGGACATGATACCAAGAACACAACTTACAGCTTGAGGGGGGTGTT 188  
 QY 61 AlaleuValThralaValCysCysLeuAlaAspGlyAlaLeuIleTyraTglsLeu 80  
 Db 187 GCATTGTGACAGAGATGCTGCTGCGACGGGGCCCTTTATTCGGAAGCTTCTG 128

RESULT 8  
 LOCUS A1128804 423 bp mRNA linear EST 05-OCT-1998  
 DEFINITION q94d08.s1 Soares\_fetal\_heart\_NbH19W Homo sapiens CDNA clone  
 IMAGE:1694391 3', mRNA sequence.  
 ACCESSION A1128804  
 VERSION A1128804.1 GI:3597318  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 423)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnln.gov) for further information.  
 Insert length: 382 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amerisham  
 High quality sequence stop: 413.  
 Location/Qualifiers  
 source 1..423  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="1694391"  
 /clone\_lib="Soares\_fetal\_heart\_NbH19W"  
 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: heart; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site: 1: Not I; Site: 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTACCAATTCGACAGTGGAGCGCGCATCTTTTATTTTATTTT 3']  
 TGTACCAATTCGACAGTGGAGCGCGCATCTTTTATTTTATTTT 3']  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by  
 M. Fatima Bonaldo. This library was constructed from the  
 same fetus as the fetal lung library, Soares fetal lung  
 NbH19W."

BASE COUNT 116 a 101 c 89 g 117 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.66e-59 Length: 423  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x A1128804 (1-423)

QY 1 MetaspasnaValGlnProLysIleLysHisArgProPhcCysPheSerValLysGlyHis 20

Db	353	ATGGATAACGTCACACCCAAAAATAAACAATGCGCCCTTGCTGATCGTGAAGGCCAC	294
QY	21	VallYMeCLeuAlArgLeuAspIleIeKnsSerIeuValThrThrValPheMeIleuIle	40
Db	293	GTAAGAAATGCTCGGGCTGGATATTATCAACACACTGGTAACACAGTATTCACTGCATC	234
QY	41	ValSerValIleuAlaIleuIleProGluThrThrThrLeuThrValGlyGlyIylValPhe	60
Db	233	GTATCTGCTGTGGCACTATACCAAGAAACCAACATGTGACAGTGGTGAGGGGGTGT	174
QY	61	AlaIleuValThAlaValAlCyScysLeuAlaAspGlyAlaIleuIleTyArgIylsLeuIleu	80
Db	173	GCACCTGTGACAGCAGTATGCTGTCCTTGGCCGACGGGGCCCTTATTACGGAAGCTTCG	114
QY	81	PheAsnProSerGlyProTyrglnIlybysProValHisGluIylsGlyGluValIleu	99
Db	113	TTTCATCCCGAGGGGCTCTTACAGAAAAAGCCTGTGATCAAAAAAAGAAGATTGG	57

RESULT 9					
AA455042/c	AA455042	427 bp	MRNA	linear	EST 06-JUN-1997
LOCUS	aa04a07.s1 Soares_NhHMPu_S1		Homo sapiens	CDNA clone	IMAGE:812244
DEFINITION	3', mRNA sequence.				
ACCESSION	AA455042				
VERSION	AA455042.1	GI:2177818			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
11 (bases 1 to 427)	Hillier, L., Allen, M., Bowles, L., Dubnugue, T., Getse, G., Jost, S., Kuchba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, J., Wyllie, T., Waterston, R., and Wilson, R.	WASHU-Merck EST Project 1997	Unpublished (1997)	Contact: Wilson RK

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: este@watson.wustl.edu  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -41m3 fwd. EF from Amersham  
High quality sequence stop: 395.  
Location/Qualifiers

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source
1. .42/
/organism="Homo sapiens"
/db_xref="GDB:604315"
/db_xref="taxon:9606"
/clone IMAGE:812244"
/clone_1lb="Soares_NhMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"

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(phone: 0rgan: mixed (see below) Vector: PT733D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDHM, pregnant uterus NBHPU, and fetal heart NBHHLW) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-488478.

BASE COUNT	119 a	101 c	91 g	116 t
------------	-------	-------	------	-------

ORIGIN

Alignment Scores:

Pred. No.:	4,72e-59	Length:	427
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-801-115B-2 (1-99) X AA455042 (1-427)

QY	1	MetAspAsnValGlnProLysIleLysSHisArgProPheCysPheSerValLysGlnHis	20
Db	356	ATGGATACCTGCAGCGCAAAATAAACAATCGCCCTTCCTGCATGAGTGAAGGCCAC	29
QY	21	ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle	40
Db	296	GTCAGATGCTGGCGGCTGGATATTATTCACCTCACTGGTACACACAGTATTCGTCATC	23
QY	41	ValSerValLeuAlaLeuIleLeuProGluThrThrThrLeuThrValGlyGlyValAlaPhe	60
Db	236	GATATCTGTGTGGCACTGATACACGAACACACAACATTGACAGTGGTGAGAGCGCTGTTT	17
QY	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu	80
Db	176	GCACCTGTGCACACAGTATGCTGTCTTCGGCAGAGGGGCCCTTATTACCGAAGCTTCTG	11
QY	81	PheAsnProSerLysProTyrGlnLysLysProValHisGlnLysGlyValLeu	99
Db	116	TTCAATCCACGCGGCTCTTACACGAAAAAGCGCTGCACGAAAAAAGAAAGAAATTTTTC	60

RESULT 10	432 bp	mRNA	linear	EST 16-OCT-1994
AA429945/c				
LOCUS	2667710..s1	Soares-testis_NHT	Homo sapiens	cdna IMAGE:781291
DEFINITION	3', mRNA sequence.			
ACCESSION	AA429945			
VERSION	AA429945			
KEYWORDS	AA429945.1	GI:2113244		
EST.				
SOURCE	human.			
ORGANISM	Homo sapiens			

REFERENCE	Mkayroya; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (pases 1 to 433)
AUTHORS	Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaca, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, S., Schellenberg, K., Stepien, M., Tan, F., Theisling, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE	WashU-Merck EST Project 1997
JOURNAL	Unpublished (1997)
COMMENT	Contact: Wilson RK

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewartson.wustl.edu  
This clone is available royalty-free through LILN; contact the  
IMAGE Consortium (info@image.jhmi.gov) for further information.  
Seq primer: -14m13 fwd. ET from Amerham  
High quality sequence from 421

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FEATURES
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    Location/Qualifiers
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      /db_xref="taxon:9606"
      /clone="IMAGE:781291"
      /clone_lib="Scares_testis_NHT"
      /sex="male"
      /lab_host="DH10B"
      /note="Vector: pRTT3p-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
cDNA"

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was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5'

5'-TGTTACCAATCTGAAGTGGAGAGGGCCGCCCAATTTTTTTTTTTT 3'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not

and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot's, and was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT

119 a 101 c 92 g 120 t

were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 26032-26523, 340488-345479, and 484488-489479. "

ORIGIN

BASE COUNT

125 a 110 c 97 g 120 t

Alignment Scores:

Alignment Scores:

Pred. No.: 4.8e-59 Length: 432  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

Pred. No.: 5.12e-59 Length: 452  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-801-115b-2 (1-99) x AA429945 (1-432)

QY 1 MetaspasnaValGlnProLysIleLysHisArgProPhcysPheSerValLysGlyHis 20

Db 361 ATGATACGTCGCGCGGAAATTAACATCGCCCTTCCTTCAGTGTGAAGGCCAC 302

QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40

Db 301 GTGAGATGCTGCGCGGATATATCACTGCTGTAACACAGATTCATGCTCATC 242

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60

Db 241 GTACTGTGTGGACGATACGATACGAAACCAACATTCAGTGTGAGGGGTCTT 182

QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80

Db 181 GCACCTGTGACAGAGATGCTGCTGCCGACGCGGCCCTTATTACCGGAACCTCTG 122

QY 81 PheAsnProSerGlyProTyrGlnLysIleLysIleGluValLysGlyValLeu 99

Db 121 TTCATCCACGCGCTCTTACCAAGAAAGCCGTGATGATGAAAGAGTTTG 65

QY 81 PheAsnProSerGlyProTyrGlnLysIleLysIleGluValLysGlyValLeu 99

Db 121 TTCATCCACGCGCTCTTACCAAGAAAGCCGTGATGATGAAAGAGTTTG 65

QY 81 PheAsnProSerGlyProTyrGlnLysIleLysIleGluValLysGlyValLeu 99

Db 121 TTCATCCACGCGCTCTTACCAAGAAAGCCGTGATGATGAAAGAGTTTG 65

QY 81 PheAsnProSerGlyProTyrGlnLysIleLysIleGluValLysGlyValLeu 99

Db 121 TTCATCCACGCGCTCTTACCAAGAAAGCCGTGATGATGAAAGAGTTTG 65

QY 81 PheAsnProSerGlyProTyrGlnLysIleLysIleGluValLysGlyValLeu 99

Db 121 TTCATCCACGCGCTCTTACCAAGAAAGCCGTGATGATGAAAGAGTTTG 65

QY 81 PheAsnProSerGlyProTyrGlnLysIleLysIleGluValLysGlyValLeu 99

Db 121 TTCATCCACGCGCTCTTACCAAGAAAGCCGTGATGATGAAAGAGTTTG 65

QY 81 PheAsnProSerGlyProTyrGlnLysIleLysIleGluValLysGlyValLeu 99

Db 121 TTCATCCACGCGCTCTTACCAAGAAAGCCGTGATGATGAAAGAGTTTG 65

QY 81 PheAsnProSerGlyProTyrGlnLysIleLysIleGluValLysGlyValLeu 99

Db 121 TTCATCCACGCGCTCTTACCAAGAAAGCCGTGATGATGAAAGAGTTTG 65

QY 81 PheAsnProSerGlyProTyrGlnLysIleLysIleGluValLysGlyValLeu 99

Db 121 TTCATCCACGCGCTCTTACCAAGAAAGCCGTGATGATGAAAGAGTTTG 65

QY 81 PheAsnProSerGlyProTyrGlnLysIleLysIleGluValLysGlyValLeu 99

Db 121 TTCATCCACGCGCTCTTACCAAGAAAGCCGTGATGATGAAAGAGTTTG 65

QY 81 PheAsnProSerGlyProTyrGlnLysIleLysIleGluValLysGlyValLeu 99

Db 121 TTCATCCACGCGCTCTTACCAAGAAAGCCGTGATGATGAAAGAGTTTG 65

QY 81 PheAsnProSerGlyProTyrGlnLysIleLysIleGluValLysGlyValLeu 99

Db 121 TTCATCCACGCGCTCTTACCAAGAAAGCCGTGATGATGAAAGAGTTTG 65

QY 81 PheAsnProSerGlyProTyrGlnLysIleLysIleGluValLysGlyValLeu 99

Db 121 TTCATCCACGCGCTCTTACCAAGAAAGCCGTGATGATGAAAGAGTTTG 65

QY 81 PheAsnProSerGlyProTyrGlnLysIleLysIleGluValLysGlyValLeu 99

Db 121 TTCATCCACGCGCTCTTACCAAGAAAGCCGTGATGATGAAAGAGTTTG 65



451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: mscores@blue.weeg.uiowa.edu

The sequence contained an oligo-dt track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab clone distribution: clones will be available through Research Genetics (www.resgen.com)  
Seq primer: M13 Forward  
POLA-Res.

#### FEATURES

##### source

1. 510  
Location/Qualifiers  
/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-CAL-b12-0-UI"  
/lab\_host="UI-R-CAL"  
/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-CAL library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at [ratist.eng.uiowa.edu](http://ratist.eng.uiowa.edu). The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)  
TAG\_SEQ=None found"

BASE COUNT 130 a 131 c 104 g 145 t  
ORIGIN

#### Alignment Scores:

Pred. No.: 6,09e-59 Length: 510  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-801-115B-2 (1-99) x BF399486 (1-510)

QY 1 Metaspasnavalglnprolysilleyshisargprophycyspheservallyslyhis 20  
DB 371 ATGGATACGTGCAGCCGAAATAAATCAATCGCCCTCTGCTTCAGTGAAGGCCAC 312  
QY 21 Vallysmetleuargleuaspllelleasnserleuvalthrthrvalphemetleu 40  
DB 311 GTGAAGATGCTGCGGCTGGATATTATCACTGCTGTAACACAGATATTCATCTCATC 252  
QY 41 ValserValleualaleuileproglutthrthrleuthrvalgllygllyvalphe 60  
DB 251 GTATCTGTGTGGCACTATACAGAAACCAACATTCAGTGGTGGAGGGGTGTTT 192  
QY 61 Alaleuvalthrvalalacyscysleualaasplyalaleuiletyrarglyleu 80  
DB 191 GCACCTGTGACAGAGATGCTGCTTGCACGCGGGCCCTTATTATCCGGAAGCTCTG 132  
QY 81 Pheasnproserglyprotyrglnlylsysprovalhisgulylsysgluvalleu 99  
DB 131 TTCATTCACGCGGTCTTACCAAGAAAAGCCTGTGCAAAAAAAGAGTTTGTG 75

#### RESULT 15

LOCUS 524 bp mRNA linear EST 07-MAY-2001  
DEFINITION 602687808P1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:4820568 5',  
mRNA sequence.

ACCESSION BG705303  
VERSION BG705303.1 GI:13979504  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 524)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov

Tissue Procurement: MIKLOS Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LLM10725 row: 0 column: 01  
High quality sequence stop: 521.

#### FEATURES

##### source

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Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4820568"  
/clone\_id="NIH\_MGC\_95"  
/tissue\_type="hippocampus"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcag)  
); Oligo-UT primed using primer 5'-TTTTTTTTTTTTTTT-3',  
size-selected for average insert size 2.5 kb and  
normalized to R0F 5. This is a primary library enriched  
for full-length clones and constructed using the  
Cap-trapper method (Carninci, in preparation). Library  
constructed by M. Brownstein (NIH/NHGRI, National  
Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 142 a 133 c 138 g 131 t  
ORIGIN

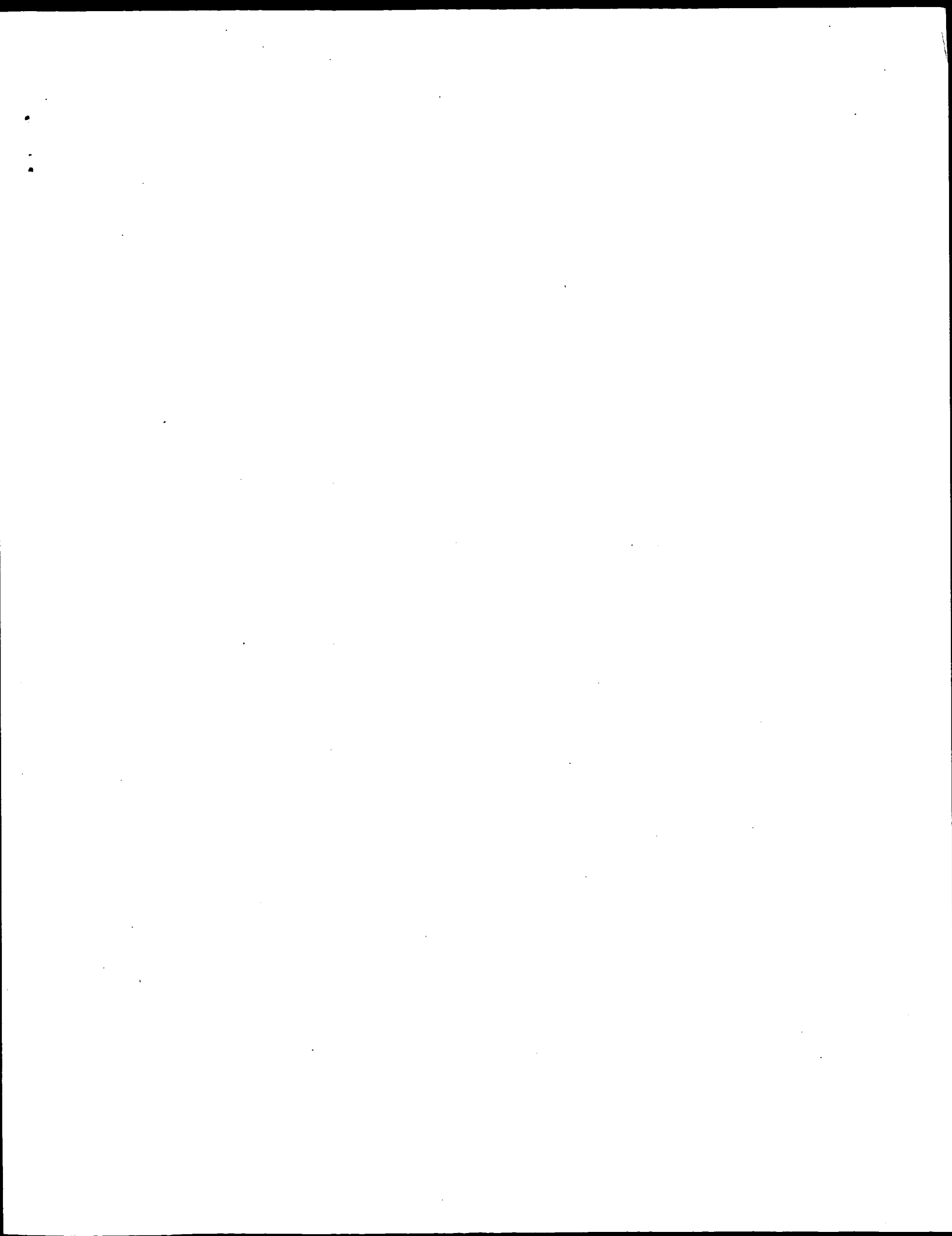
#### Alignment Scores:

Pred. No.: 6,33e-59 Length: 524  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-801-115B-2 (1-99) x BG705303 (1-524)

QY 1 Metaspasnavalglnprolysilleyshisargprophycyspheservallyslyhis 20  
DB 141 ATGGATACGTGCAGCCGAAATAAATCAATCGCCCTTCTGCTTCAGTGAAGGCCAC 200  
QY 21 Vallysmetleuargleuaspllelleasnserleuvalthrthrvalphemetleu 40  
DB 201 GTGAAGATGCTGCGGCTGGATATTATCACTGCTGTAACACAGATATTCATGCTCATC 260  
QY 41 ValserValleualaleuileproglutthrthrleuthrvalgllygllyvalphe 60  
DB 261 GTATCTGTGTGGCACTATACAGAAACCAACATTCAGTGGTGGAGGGGTGTTT 320  
QY 61 Alaleuvalthrvalalacyscysleualaasplyalaleuiletyrarglyleu 80  
DB 321 GCACCTGTGACAGAGATGCTGCTTGCACGCGGGCCCTTATTATCCGGAAGCTCTG 380  
QY 81 Pheasnproserglyprotyrglnlylsysprovalhisgulylsysgluvalleu 99  
DB 381 TTCATTCACGCGGTCTTACCAAGAAAAGCCTGTGCAAAAAAAGAGTTTGTG 437

Search completed: June 25, 2003, 13:38:30  
Job time: 1425 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 25, 2003, 11:54:40 ; Search time 215 Seconds

(without alignments)  
1036.967 Million cell updates/sec

Title: US-09-801-115B-2  
Perfect score: 508  
Sequence: 1 MDWVQPKIRKHPFCFSYKCH.....LFNPSGPKYKKPHEKKEVL 99

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODBL-frame+ p2n model -DEV-xlp  
-Q/cgn2.1/USPFO.spool/us09801115/runat\_20062003\_141102\_13575/app\_query.fasta.1.263  
-DB-Geneseq\_101002 -QFMT-fastap -SUFFIX-rng -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.cdl  
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-MODE-LOCAL -OUTFMT=pro -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO\_MMAP -LARGESOURCY -NEG\_SCORES=0 -NMT -DSPBLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

N.Geneseq.101002:\*  
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2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	508	100.0	413	20	AAK97873	Human secreted pro
2	508	100.0	439	24	ABK36006	CDNA sequence #397
3	508	100.0	504	19	AAV59598	Human secreted pro
4	508	100.0	506	19	AAV59746	Human secreted pro
5	508	100.0	515	21	AAK87730	Human secreted pro
6	508	100.0	515	22	AAK64012	CDNA encoding huma
7	508	100.0	534	21	AAK38006	CDNA encoding huma
8	508	100.0	538	22	AAK98515	Human EST-derived
9	508	100.0	538	22	AAK98548	Human EST-derived
10	508	100.0	558	22	AAK34835	Human colon cancer
11	508	100.0	655	22	AAK44932	CDNA encoding nove
12	504	99.2	297	21	AAK15919	Human protein clon
13	504	99.2	467	21	AAK15929	Human protein clon
14	489	96.3	500	20	AAK97826	Human secreted pro
15	471.5	92.8	459	21	AAK38007	CDNA encoding huma
16	471.5	92.8	637	21	AAK56747	Human transmembran
17	471.5	92.8	663	20	AAK34051	Human PRO772 nucle
18	471.5	92.8	663	21	AAK78498	Human PRO772 (UNQ4
19	471.5	92.8	663	21	AAK58238	Human secreted pro
20	471.5	92.8	669	21	AAK87771	Human secreted pro
21	471.5	92.8	669	22	AAK64053	CDNA encoding huma
22	471.5	92.8	670	24	ABK90366	Human polynucleoti
23	471.5	92.8	908	22	AAK44933	CDNA encoding nove
24	467.5	92.0	638	24	ABK35884	CDNA sequence #275
25	461	90.7	415	21	AAK00147	Human secreted pro
26	357	70.3	392	21	AAK16090	Human colon cancer
27	339.5	66.8	363	21	AAK38009	CDNA encoding nove
28	339.5	66.8	566	22	AAK45120	CDNA encoding nove
29	339.5	66.8	566	22	AAK45121	CDNA encoding nove
30	331	65.2	204	21	AAK38008	CDNA encoding nove
31	323	63.6	331	20	AAK97651	Extended human sec
32	318.5	62.7	495	20	AAK34052	Human EST DNA43509
33	318.5	62.7	495	21	AAK78499	Human EST DNA43509
34	318.5	62.7	495	22	AAK93358	CDNA encoding SRT
35	317	62.4	334	20	AAK41509	Human secreted pro
36	294	57.9	379	21	AAK41312	Human secreted exp
37	257.5	50.7	465	22	ABK09082	Human transmembran
38	245	48.2	207	24	ABK94246	Gene #744 used to
39	245	48.2	207	24	ABK62782	Breast cancer rela
40	245	48.2	207	24	ABK62959	Breast cancer rela
41	245	48.2	207	24	ABK63180	Breast cancer rela
42	215	42.3	2953	22	AAK68359	Human immune/haema
43	215	42.3	2953	22	AAK68360	Human immune/haema
44	211	41.5	13744	22	AAK68361	Human immune/haema
45	211	41.5	13744	22	AAK82406	Human immune/haema

## ALIGNMENTS

RESULT 1  
AAK97873 standard; CDNA: 413 BP.

AAK97873;  
23-SEP-1999 (first entry)

Human secreted protein encoding CDNA #61.

Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;  
diagnostic; gene therapy; chromosome mapping; secretion vector; ss.

Homo sapiens.

WO9925825-A2.

27-MAY-1999.

XX PF 13-NOV-1998; 98MO-IB01862.  
 XX PR 04-SEP-1998; 98US-0099273.  
 XX PR 13-NOV-1997; 97US-0066677.  
 XX PR 17-DEC-1997; 97US-0069957.  
 XX PR 09-FEB-1998; 98US-0074121.  
 XX PR 13-APR-1998; 98US-0081563.  
 XX PR 10-AUG-1998; 98US-0096116.  
 XX PA (GEST ) GENSET.  
 XX PI Bougueleret L, DucJert A, Dumas Milne Edwards J;  
 XX DR WPI; 1999-347472/29.  
 XX DR P-PSDB; AAY36189.  
 XX XX  
 XX PT Extended cDNAs encoding secreted proteins  
 XX PS Claim 1; Page 261; 307pp; English.  
 XX CC AAY37813-X97906 represent extended cDNA's which encode novel human  
 CC secreted proteins (see AAY36129-Y36222) and which have cytosolic,  
 CC thrombotic and osteopathic activity. The extended cDNAs can be used to  
 CC express secreted proteins or parts of them or to obtain antibodies  
 CC capable of binding to the secreted proteins. They may also be used in  
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 CC Uses also include design of expression vectors and secretion vectors.  
 XX CC  
 XX SQ Sequence 413 BP; 121 A; 82 C; 95 G; 115 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 7.04e-58 Length: 413  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0  
 US-09-801-115B-2 (1-99) x AAY37873 (1-413)  
 QY 1 MetaspasValGlnProLysIleLysHsArpProPhcysPheSerValIlyGlyHis 20  
 DB 46 ATGATTAACGTCGACGCCGAAATTAACATGCCCCCTTCTGCTTCAAGTGAAGGCCAC 105  
 QY 21 ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40  
 DB 106 GTGAAGATGCTGCGGCTGGATATTATCACTCACTGGTAACAACAGATTATCATGCTCATC 165  
 QY 41 ValSerValIleuAlaLeuIleIleProGluThrThrThrIleuThrValIglyIglyValPhe 60  
 DB 166 GTATCTGTGTGGACAGTATACAGAAACCAACCAATTTGACAGTTGGTGAAGGGGTGTTT 225  
 QY 61 AlaLeuValThrAlaValAlaCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu 80  
 DB 226 GCACTTGTGACAGAGATAGTGTGCTTCCGACAGGGGCCCTTATTATCCGGAAGCTTCTG 285  
 QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99  
 DB 286 TTCAATCCCAAGCGGTCTTACACAGAAAGCGCTGTGATGATAAAAAAGAGTTTTC 342  
 RESULT 2  
 ID ABR36006 standard; cDNA; 439 BP.  
 AC ABR36006;  
 XX  
 XX 08-MAY-2002 (first entry)  
 DT  
 XX cDNA sequence #397 encoding novel human secreted protein.  
 DE  
 XX Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
 KW Immune deficiency disorder; blood disorder; inflammatory disorder.

KW KW Infectious disorder; allergic condition; neurodegenerative disorder;  
 KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;  
 KW tumour; cancer; hepatotropic; immunosuppressive; antineumatic; gene; ss.  
 XX  
 XX OS Homo sapiens.  
 XX MO200177289-A2.  
 XX  
 XX PD 18-OCT-2001.  
 XX PF 29-MAR-2001; 2001MO-US10232.  
 XX PR 06-APR-2000; 2000US-195605P.  
 XX PA (GEMY ) GENETICS INST INC.  
 XX PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
 PI Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;  
 PI Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;  
 XX DR WPI; 2002-179322/23.  
 XX  
 XX PT Six hundred and twenty three polynucleotides derived from a variety of  
 PT human tissue sources which encode secreted proteins, useful for  
 PT treating immune deficiencies and disorders such as autoimmune disorders  
 PS Claim 1; Page 296-297; 393pp; English.  
 XX  
 XX CC The present invention relates to the isolation of novel cDNA sequences  
 CC which encode human secreted proteins. The cDNA sequences have been  
 CC derived from a variety of human tissues. The invention also provides  
 CC a method for producing proteins from these polynucleotide sequences.  
 CC The proteins are useful for identifying compounds that modulate their  
 CC activity and production. The sequences of the invention are  
 CC useful for treating diseases such as hyperproliferative disorders  
 CC (e.g. cancer), immune deficiency disorders (e.g. severe combined  
 CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple  
 CC sclerosis), blood disorders (e.g. thrombocytopenia), inflammatory  
 CC disorders (e.g. arthritis), infectious disorders (e.g. hepatitis),  
 CC allergic conditions (e.g. asthma), neurodegenerative disorders (e.g.  
 CC Alzheimer's disease), liver fibrosis, coagulation disorders (e.g.  
 CC haemophilia), and tumours. The polynucleotide sequences of the  
 CC invention are also useful in gene therapy. ABR3610-ABR36232 represent  
 CC the cDNA sequences of the invention that encode for novel human  
 CC secreted proteins.  
 XX  
 XX SQ Sequence 439 BP; 117 A; 96 C; 104 G; 122 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 7.64e-58 Length: 439  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0  
 US-09-801-115B-2 (1-99) x ABR36006 (1-439)  
 QY 1 MetaspasValGlnProLysIleLysHsArpProPhcysPheSerValIlyGlyHis 20  
 DB 81 ATGATTAACGTCGACGCCGAAATTAACATGCCCCCTTCTGCTTCAAGTGAAGGCCAC 140  
 QY 21 ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40  
 DB 141 GTGAAGATGCTGCGGCTGGATATTATCACTCACTGGTAACAACAGATTATCATGCTCATC 200  
 QY 41 ValSerValIleuAlaLeuIleIleProGluThrThrThrIleuThrValIglyIglyValPhe 60  
 DB 201 GTATCTGTGTGGACAGTATACAGAAACCAACCAATTTGACAGTTGGTGAAGGGGTGTTT 260  
 QY 61 AlaLeuValThrAlaValAlaCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu 80



DB 261 GCACCTGTGACAGCAGTATGCTGTGCGACGAGGCCCTTATTACCGAAGCTCTG 320  
QY 81 PheasnProSerGlyProTyrGlnLysPyrValHisGlnLysLysGlnValIleu 99  
DB 321 TTCAATCCACGAGGGTCTTACACGAAAAAGCGCTGTGATGAAAAAAGAGTTTGG 377  
RESULT 3  
AAV59598 standard: DNA; 504 BP.  
XX AAV59598;  
AC AAV59598;  
XX  
DT 06-JAN-1999 (first entry)  
XX  
DE Human secreted protein gene 88 clone HANA32.  
XX  
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;  
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
XX  
XX Homo sapiens.  
OS  
PN WO9839448-A2.  
XX  
PD 11-SEP-1998.  
XX  
PF 06-MAR-1998; 98WO-US04493.  
XX  
XX 02-OCT-1997; 97US-0061060.  
PR 07-MAR-1997; 97US-0038621.  
PR 07-MAR-1997; 97US-0040161.  
PR 07-MAR-1997; 97US-0040162.  
PR 07-MAR-1997; 97US-0040163.  
PR 07-MAR-1997; 97US-0040333.  
PR 07-MAR-1997; 97US-0040334.  
PR 07-MAR-1997; 97US-0040336.  
PR 07-MAR-1997; 97US-0040626.  
PR 11-APR-1997; 97US-0043311.  
PR 11-APR-1997; 97US-0043312.  
PR 11-APR-1997; 97US-0043313.  
PR 11-APR-1997; 97US-0043314.  
PR 11-APR-1997; 97US-0043356.  
PR 11-APR-1997; 97US-0043359.  
PR 11-APR-1997; 97US-0043376.  
PR 11-APR-1997; 97US-0043578.  
PR 11-APR-1997; 97US-0043580.  
PR 11-APR-1997; 97US-0043670.  
PR 11-APR-1997; 97US-0043671.  
PR 11-APR-1997; 97US-0043672.  
PR 11-APR-1997; 97US-0043674.  
PR 23-MAY-1997; 97US-0047492.  
PR 23-MAY-1997; 97US-0047500.  
PR 23-MAY-1997; 97US-0047501.  
PR 23-MAY-1997; 97US-0047502.  
PR 23-MAY-1997; 97US-0047503.  
PR 23-MAY-1997; 97US-0047581.  
PR 23-MAY-1997; 97US-0047582.  
PR 23-MAY-1997; 97US-0047583.  
PR 23-MAY-1997; 97US-0047584.  
PR 23-MAY-1997; 97US-0047585.  
PR 23-MAY-1997; 97US-0047586.  
PR 23-MAY-1997; 97US-0047587.  
PR 23-MAY-1997; 97US-0047588.  
PR 23-MAY-1997; 97US-0047589.  
PR 23-MAY-1997; 97US-0047590.  
PR 23-MAY-1997; 97US-0047592.  
PR 23-MAY-1997; 97US-0047593.

PR 23-MAY-1997; 97US-0047594.  
PR 23-MAY-1997; 97US-0047595.  
PR 23-MAY-1997; 97US-0047596.  
PR 23-MAY-1997; 97US-0047597.  
PR 23-MAY-1997; 97US-0047598.  
PR 23-MAY-1997; 97US-0047599.  
PR 23-MAY-1997; 97US-0047600.  
PR 23-MAY-1997; 97US-0047601.  
PR 23-MAY-1997; 97US-0047612.  
PR 23-MAY-1997; 97US-0047613.  
PR 23-MAY-1997; 97US-0047614.  
PR 23-MAY-1997; 97US-0047615.  
PR 23-MAY-1997; 97US-0047617.  
PR 23-MAY-1997; 97US-0047618.  
PR 23-MAY-1997; 97US-0047632.  
PR 23-MAY-1997; 97US-0047633.  
PR 06-JUN-1997; 97US-0048964.  
PR 13-JUN-1997; 97US-0048974.  
PR 08-JUL-1997; 97US-0049610.  
PR 16-JUL-1997; 97US-0051926.  
PR 18-AUG-1997; 97US-0052874.  
PR 22-AUG-1997; 97US-0055724.  
PR 22-AUG-1997; 97US-0056630.  
PR 22-AUG-1997; 97US-0056631.  
PR 22-AUG-1997; 97US-0056632.  
PR 22-AUG-1997; 97US-0056636.  
PR 22-AUG-1997; 97US-0056637.  
PR 22-AUG-1997; 97US-0056662.  
PR 22-AUG-1997; 97US-0056664.  
PR 22-AUG-1997; 97US-0056845.  
PR 22-AUG-1997; 97US-0056862.  
PR 22-AUG-1997; 97US-0056864.  
PR 22-AUG-1997; 97US-0056872.  
PR 22-AUG-1997; 97US-0056874.  
PR 22-AUG-1997; 97US-0056875.  
PR 22-AUG-1997; 97US-0056876.  
PR 22-AUG-1997; 97US-0056877.  
PR 22-AUG-1997; 97US-0056878.  
PR 22-AUG-1997; 97US-0056879.  
PR 22-AUG-1997; 97US-0056880.  
PR 22-AUG-1997; 97US-0056881.  
PR 22-AUG-1997; 97US-0056882.  
PR 22-AUG-1997; 97US-0056884.  
PR 22-AUG-1997; 97US-0056886.  
PR 22-AUG-1997; 97US-0056887.  
PR 22-AUG-1997; 97US-0056888.  
PR 22-AUG-1997; 97US-0056889.  
PR 22-AUG-1997; 97US-0056892.  
PR 22-AUG-1997; 97US-0056893.  
PR 22-AUG-1997; 97US-0056894.  
PR 22-AUG-1997; 97US-0056903.  
PR 22-AUG-1997; 97US-0056908.  
PR 22-AUG-1997; 97US-0056909.  
PR 22-AUG-1997; 97US-0056910.  
PR 22-AUG-1997; 97US-0056911.  
PR 05-SEP-1997; 97US-0057650.  
PR 05-SEP-1997; 97US-0057669.  
PR 05-SEP-1997; 97US-0057761.  
PR 12-SEP-1997; 97US-0058785.  
(HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;  
XX Feng P, Ferlie AM, Fischer CL, Florence KA, Greene JM, Hu JS;  
XX Ryan H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;  
XX Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;  
XX WPI; 1998-506364/43.  
XX P-PSDB; AAW74818.  
PT New isolated human genes and the secreted polypeptide(s) they encode  
PT - useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders

XX Claim 1; Page 320; 721pp; English.

XX This sequence represents a nucleic acid molecule designated Gene 88 from  
CC the human cDNA clone HAAV32 (deposited as clone ATCC 97901 and ATCC  
CC 209047) which encodes a secreted human protein. The gene can be used to  
CC generate fusion proteins by linking to the gene to a human  
CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of  
CC the fused protein as compared to the human protein only.  
CC The invention relates to 186 novel genes and their fragments (nucleic  
CC acid sequences: AAV59511-V59812; amino acid sequences AAV74731-W75026)  
CC which are useful for preventing, treating or ameliorating medical  
CC conditions e.g. by protein or gene therapy. Also, pathological conditions  
CC can be diagnosed by determining the amount of the new polypeptides in a  
CC sample or by determining the presence of mutations in the new  
CC polynucleotides. Specific uses are described for each of the 186  
CC polynucleotides, based on which tissues they are most highly expressed in  
CC (see AAV59511 for described uses).

XX Sequence 504 BP; 143 A; 106 C; 128 G; 127 T; 0 other;

XX

XX Alignment Scores:

XX Pred. No.: 9, 22e-58 Length: 504

XX Score: 508.00 Matches: 99

XX Percent Similarity: 100.00% Conservatve: 0

XX Best Local Similarity: 100.00% Mismatches: 0

XX Query Match: 100.00% Indels: 0

XX DB: 19 Gaps: 0

XX

XX US-09-801-115B-2 (1-99) x AAV59598 (1-504)

XX

XX 1 MetaspasvnaIglProlystIlelyshIsarPropheCyspSeSerVallyGlyHis 20

XX 131 ATGGATTAACCTGACCGCCGAAATATAACATCGCCCTCTGCTTCAAGTGAAGGCCAC 190

XX 21 VallyMetleuArgleuAspIleleasSerleuValThrThrValPheMetleuIle 40

XX 191 GTGAAGATGCTGCGGCTGATATTAACACGACGATGACGATTAATCATCTCATC 250

XX 41 ValSerValleuAlaIleuIleProgluThrThrThrleuThrValIleGlyIleValPhe 60

XX 251 GTATCTGTGTGGCAGCTATACAGAACCAACACATGACAGTTGGTGGAGGGGTCTT 310

XX 61 AlaIleuValThrAlaValCysCysleuAlaAspIleAlaIleuIleThrArgLysleu 80

XX 311 GCACCTGTGACAGCAGTATGCTGCTTCCGACGGGGCCCTTATTACCGGAAGCTTCTG 370

XX 81 PheasnProSerGlyProTyrgIlnlyslsProvalHIsGluLysGluValleu 99

XX 371 TTCATCCACGCGGCTTACACAGAAAGCCTGTGCTGATGAAAAAAGAGATTTC 427

XX

XX RESULT 4

XX AAV59746

XX AAV59746 standard; DNA: 506 BP.

XX

XX AAV59746;

XX

XX 19-JAN-1999 (first entry)

XX

XX Human secreted protein gene 88 clone HAAV32.

XX

XX Human: secreted protein; fusion protein; gene therapy; protein therapy;  
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
XX developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
XX immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
XX inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
XX osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX

XX Homo sapiens.

XX

XX OS

XX MO9839448-A2.

XX

XX

XX 11-SEP-1998.

XX

XX 06-MAR-1998; 98WO-US04493.

XX

XX 02-OCT-1997; 97US-0061060.

XX 07-MAR-1997; 97US-0038621.

XX 07-MAR-1997; 97US-0040161.

XX 07-MAR-1997; 97US-0040162.

XX 07-MAR-1997; 97US-0040163.

XX 07-MAR-1997; 97US-0040333.

XX 07-MAR-1997; 97US-0040334.

XX 07-MAR-1997; 97US-0040336.

XX 07-MAR-1997; 97US-0040362.

XX 11-APR-1997; 97US-0043311.

XX 11-APR-1997; 97US-0043312.

XX 11-APR-1997; 97US-0043313.

XX 11-APR-1997; 97US-0043314.

XX 11-APR-1997; 97US-0043568.

XX 11-APR-1997; 97US-0043569.

XX 11-APR-1997; 97US-0043576.

XX 11-APR-1997; 97US-0043578.

XX 11-APR-1997; 97US-0043580.

XX 11-APR-1997; 97US-0043669.

XX 11-APR-1997; 97US-0043670.

XX 11-APR-1997; 97US-0043671.

XX 11-APR-1997; 97US-0043672.

XX 11-APR-1997; 97US-0043674.

XX 23-MAY-1997; 97US-0047492.

XX 23-MAY-1997; 97US-0047500.

XX 23-MAY-1997; 97US-0047501.

XX 23-MAY-1997; 97US-0047502.

XX 23-MAY-1997; 97US-0047503.

XX 23-MAY-1997; 97US-0047581.

XX 23-MAY-1997; 97US-0047582.

XX 23-MAY-1997; 97US-0047583.

XX 23-MAY-1997; 97US-0047584.

XX 23-MAY-1997; 97US-0047585.

XX 23-MAY-1997; 97US-0047586.

XX 23-MAY-1997; 97US-0047587.

XX 23-MAY-1997; 97US-0047588.

XX 23-MAY-1997; 97US-0047589.

XX 23-MAY-1997; 97US-0047590.

XX 23-MAY-1997; 97US-0047592.

XX 23-MAY-1997; 97US-0047593.

XX 23-MAY-1997; 97US-0047594.

XX 23-MAY-1997; 97US-0047595.

XX 23-MAY-1997; 97US-0047596.

XX 23-MAY-1997; 97US-0047597.

XX 23-MAY-1997; 97US-0047598.

XX 23-MAY-1997; 97US-0047599.

XX 23-MAY-1997; 97US-0047600.

XX 23-MAY-1997; 97US-0047601.

XX 23-MAY-1997; 97US-0047612.

XX 23-MAY-1997; 97US-0047613.

XX 23-MAY-1997; 97US-0047614.

XX 23-MAY-1997; 97US-0047615.

XX 23-MAY-1997; 97US-0047617.

XX 23-MAY-1997; 97US-0047618.

XX 23-MAY-1997; 97US-0047632.

XX 23-MAY-1997; 97US-0047633.

XX 06-JUN-1997; 97US-0048964.

XX 06-JUN-1997; 97US-0048974.

XX 13-JUN-1997; 97US-0049610.

XX 08-JUL-1997; 97US-0051926.

XX 16-JUL-1997; 97US-0052874.

XX 18-AUG-1997; 97US-0053724.

XX 22-AUG-1997; 97US-0056630.

XX 22-AUG-1997; 97US-0056631.

XX 22-AUG-1997; 97US-0056632.

XX 22-AUG-1997; 97US-0056636.

XX 22-AUG-1997; 97US-0056637.

XX 22-AUG-1997; 97US-0056662.

PR 22-AUG-1997; 97US-0056664.  
 PR 22-AUG-1997; 97US-0056845.  
 PR 22-AUG-1997; 97US-0056862.  
 PR 22-AUG-1997; 97US-0056862.  
 PR 22-AUG-1997; 97US-0056872.  
 PR 22-AUG-1997; 97US-0056874.  
 PR 22-AUG-1997; 97US-0056875.  
 PR 22-AUG-1997; 97US-0056876.  
 PR 22-AUG-1997; 97US-0056877.  
 PR 22-AUG-1997; 97US-0056878.  
 PR 22-AUG-1997; 97US-0056879.  
 PR 22-AUG-1997; 97US-0056880.  
 PR 22-AUG-1997; 97US-0056881.  
 PR 22-AUG-1997; 97US-0056882.  
 PR 22-AUG-1997; 97US-0056884.  
 PR 22-AUG-1997; 97US-0056886.  
 PR 22-AUG-1997; 97US-0056887.  
 PR 22-AUG-1997; 97US-0056888.  
 PR 22-AUG-1997; 97US-0056889.  
 PR 22-AUG-1997; 97US-0056892.  
 PR 22-AUG-1997; 97US-0056893.  
 PR 22-AUG-1997; 97US-0056894.  
 PR 22-AUG-1997; 97US-0056903.  
 PR 22-AUG-1997; 97US-0056908.  
 PR 22-AUG-1997; 97US-0056909.  
 PR 22-AUG-1997; 97US-0056910.  
 PR 22-AUG-1997; 97US-0056911.  
 PR 05-SEP-1997; 97US-0057650.  
 PR 05-SEP-1997; 97US-0057669.  
 PR 05-SEP-1997; 97US-0057761.  
 PR 12-SEP-1997; 97US-0058785.

## (HUMA-) HUMAN GENOME SCI INC.

XX Bednarik DP, Brewer LA, Carter KC, Duan R, Edner R, Endress GA;  
 PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;  
 PI Kyah H, Lafleur DM, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;  
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;  
 DR MPI: 1998-506364/43.  
 DR P-PSDB: AAW74961.

XX New isolated human genes and the secreted polypeptide(s) they encode  
 PT - useful for diagnosis and treatment of e.g. cancers, neurological  
 PT disorders, immune diseases, inflammation or blood disorders

XX Claim 1; Page 472; 721pp; English.

XX This sequence represents a nucleic acid molecule designated Gene 88 from  
 CC the human CDNA clone HANAV32 (deposited as clone ATCC 97897 and ATCC  
 CC 209043) which encodes a secreted human protein. The gene can be used to  
 CC generate fusion proteins by linking to the gene to a human  
 CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of  
 CC the fused protein as compared to the human protein only.  
 CC The invention relates to 186 novel genes and their fragments (nucleic  
 CC acid sequences: AAV59511-595812; amino acid sequences AAW74731-W75026)  
 CC which are useful for preventing, treating or ameliorating medical  
 CC conditions e.g. by protein or gene therapy. Also, pathological  
 CC conditions can be diagnosed by determining the amount of the new  
 CC polypeptides in a sample or by determining the presence of mutations in  
 CC the new polynucleotides. Specific uses are described for each of the 186  
 CC polynucleotides, based on which tissues they are most highly expressed in  
 CC (see AAV59511 for described uses).

XX Sequence 506 BP; 148 A; 103 C; 121 G; 132 T; 2 other;

## Alignment Scores:

Pred. No.: 9,27e-58 Length: 506  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 19 Gaps: 0

US-09-801-115B-2 (1-99) x AAV59746 (1-506)

QY 1 MetAspAsnValGlnProlystlelyshsArgProphCysPheSerVallysglyhs 20  
 Db 117 ATGGATVACGTGACGCGAAATATAAACATVCCCTCTGCTGCTGTAAGGCCAC 176  
 QY 21 VallyMetleuArgleuaspilleleasenserieValThrThValPheMetleulle 40  
 Db 177 GTCAATATGCTGGCGGTGATATATACATCTACGTGTACACAGTATCTGCTATC 236  
 QY 41 ValSerValleuAlaleuileProgluThrThrleuThValGlyGlyValPhe 60  
 Db 237 GTATCTGTGTGACATGATACAGAAACACACATGACAGTTGCTGAGGCGTGT 296  
 QY 61 AlaleuValThrAlaValCysCysleuAlaaspGlyAlaLeuileTyraRgPstleu 80  
 Db 297 GCACCTGTGACACAGTATGCTGTCTGCGACGGGCGCTTATTTACCGAAGCTTCTG 356  
 QY 81 PheAsnProSerGlyProTyrglnlylsProValHisGluLysGluValleu 99  
 Db 357 TTCAATCCAGCGGTCTTACAGAAAGCCGTGTCATGAAAAAAGAAAGTTTG 413

## RESULT 5

AAA87730 standard; cDNA; 515 BP.

AAA87730;

28-NOV-2000 (first entry)

Human secreted protein encoding cDNA SEQ ID #29.

XX Human: secreted protein; forensic procedure; gene therapy;  
 KW chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;  
 KW cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;  
 KW brain disorder; skeletal muscle disorder; eye disorder; obesity;  
 KW mitochondrialcytopathy; diabetes; atherosclerosis; Alzheimer's disease;  
 KW neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;  
 KW septic shock; impotence; ss.

XX Homo sapiens.

XX WO200037491-A2.

XX 29-JUN-2000.

XX 20-DEC-1999; 99WO-IB02058.

XX 22-DEC-1998; 98US-0113686.

XX 25-JUN-1999; 99US-0141032.

XX (GEST) GENSET.

XX Bougueleret L, Dumas J, Duclert A;

XX MPI: 2000-442637/38.

XX P-PSDB: AAB25768.

XX Polynucleotides and polypeptides encoding proteins with signal  
 PT peptides, useful in diagnostic, forensic, gene therapy and chromosome  
 PT mapping procedures -

XX Claim 1; Page 169-170; 306pp; English.

XX This sequence represents human cDNA encoding a secreted protein. The  
 CC invention relates to sequences AAA87725-AA87774 which encode human  
 CC secreted proteins AAB25763-B25812. The proteins include signal peptides.  
 CC Included in the invention are a host cell containing one of the cDNA  
 CC sequences, and a purified antibody capable of binding to one of the  
 CC secreted proteins. Also contained in the invention are methods for  
 CC storing the sequence data on a computer system, and a method for  
 CC identifying features of the cDNA sequences using a computer programme.

CC The cDNAs are useful for expressing secreted proteins or fragments to  
CC obtain antihodies capable of specifically binding to the secreted  
CC proteins. The cDNAs may also be useful in diagnostic, forensic, gene  
CC therapy and chromosome mapping procedures and may be used to design  
CC expression vectors and secretion vectors. The proteins of the invention  
CC may be used to treat diseases including cancer, autoimmune diseases,  
CC cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological  
CC disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye  
CC disorders, obesity, mitochondrialcytopathies, diabetes, atherosclerosis,  
CC neurodegenerative disorders, graft rejection, Alzheimer's disease,  
CC dementia, hyperlipidaemia, septic shock and impotence.

Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

**Alignment Scores:**

Pred. No.:	5,49e-58	Length:	515
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-801-115B-2 (1-99) x AAA87730 (1-515)

QY	1	MeAspAsnValGlnProIysIleIysHisArgProPheCysPheSerValIleGlyHis	20
Db	144	ATGGATTACGCTGCACGCCAAATAAACAATGCCCCCTCTCTGTTACAGTGAAGAAGGCCAC	203
QY	21	ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle	40
Db	204	GTTGAATGCTCGCGCTGATATTATCACTCAGTGTACACAGATTATCATCTATC	263
QY	41	ValSerValLeuAlaLeuIleProGlnThrThrPheLeuThrValGlyGlyValPhe	60
Db	264	GATCTGTTGGCACTGTATACCAAAACCAACAAATTGACAGTGGGGAGGGGTGTT	323
QY	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgIysLeuIleu	80
Db	324	GCACCTGTACAGCAGTATGCTGCTTGGCCAGCGGGCCCTTATTTACCGGAAGCTCTGG	383
QY	81	PheAsnProSerGlyProCysGlnIleIysProValHisGlyIysGlyValLeu	99
Db	384	TTCAATCCACGGGGCTCTTACCAAGAAAGCCTGTGCATGAAAAAAGAAAGATTGG	440

RESULT 6  
AAAF64012  
ID AAAF64012 standard; cDNA; 515 bp

AC AAF64012;

DT 05-APR-2001 (first entry)

CDNA encoding human secreted protein #13.

**KW** Secreted protein; prevention; treatment; diagnosis; disease;

KW Intection; ds

PN WO200100806-A2.

PD 04-JAN-2001.

PF 21-JUN-2000; 2000WO-IB00951.

PR 25-JUN-1999; 99US-0141032.

PR 21-DEC-1999; 99US-0469099.

PA (GEST ) GENSET.

PI Dumas Milne Edwards J, Bougueleret L, Jobert S,

DR WPI; 2001-071487/08

XX 49 Secreted proteins and the nucleic acids encoding them, useful in  
PT gene therapy and for detecting similar sequences in samples -  
XX  
PS Claim 1; Page 225; 307pp; English.

CC The present invention relates to 49 secreted proteins and the cDNAs  
CC encoding them. The protein and nucleic acids may be used in the  
CC prevention, treatment and diagnosis of diseases associated with  
CC inappropriate protein expression.

SQ Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other,

Alignment Scores:

Score, No.:	5.49e-58	length:	515
Percent Similarity:	908.00	Matches:	99
Best Local Similarity:	100.00%	Conservative:	0
Query Match:	100.00%	Mismatches:	0
DB:	22	Indels:	0
		Gaps:	0

US-09-801-115B-2 (1-99) X AAF64012 (1-515)

OY	1	MetAspAsnValGlnProIysIleYshAspProPheCysPheSerValIysGlyHis	20
Db	144	ATGGATTAACGTGCAGCCGAAATAAACAATGCCCCCTTCTGCTTACGTGTAAAGGCCAC	203
OY	21	ValIysMetIeuAArgIeuAspIleIleAsnSerIeuValThrThrValPheMetIeuIle	40
Db	204	GTAACAATGCTGCCTCGATATTATTAACAATCACTACAGGTAAACAACGATATCATCTCATC	263
OY	41	ValSerValIeuAlaIeuIleProGluThrThrThrIleuThrValGlyGlyValPhe	60
Db	264	GATCTGTGTGGCACTGATACCAAGAAACACAAATTAAGACAGTGGGAGGGGGTGT	322
OY	61	AlaIeuValThrAlaValAlcCysCysIeuAlaAspGlyAlaIeuIleTyrArgIysIeuIeu	80
Db	324	GCACTGTGCACAGCAATATGCTGTCTTCGGCAGCGGGCCCTTATTTACCGGAACCTCTG	383
OY	81	PheAsnProSerGlyProTyrGlnIlyIysProValHisGlyIysGlyValIeu	99
Db	384	TTCAATCCACAGCGGCTCTTACCAAGAAAAGCCTGTGCATGAAAAAAAAGAGTTTGG	440

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RESULT 7
AAA38006
ID    AAA38006 standard; cDNA; 534 BP

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AC AAA38006;

DT 22-AUG-2000 (first entry)

DE UCK-1 nucleotide sequence.

KW UCK-1; chemotaxis factor; immunocyte; haemopoiesis stimulant; tumour;  
radiotherapy; chemotherapy; human; ss.

•

XX

PN CN1244584-A

PD 16-FEB-2000.

PF 14-MAY-1999; 99CN-0107284.

PR 14-MAY-1999; 99CN-0107284.

PA (UYBE-) UNIV BEIJING MEDICAL.

PI Ma D, Han W, Zhang Y;

DR WPI; 2000-388170/34.

DK P-PSDB; AAY98142  
XX

PT	Chemotactic factor useful for treatment and diagnosis of immunocyte
PT	disorders - has immunocyte chemotactic stimulating factor
PT	

PS Example 4; Fig 1; 31pp; Chinese.

CC This sequence represents an UCK-1 cDNA sequence encoding a chemotaxis  
CC factor polypeptide. The UCK-1 protein exhibits immunocyte chemotaxis  
CC activity and a haemopoietic stimulating effect. The invention relates to  
CC UCK proteins, their encoding nucleotide sequences and antibodies and  
CC antagonists against the proteins. The nucleotide and protein sequences  
CC are useful for the preparation of a composition for the diagnosis and  
CC treatment of diseases associated with abnormal immunocyte function and  
CC low haemopoiesis function caused by radiotherapy and chemotherapy used to  
CC treat tumours and other diseases.

**Sequence** 534 BP; 156 A; 110 C; 134 G; 134 T; 0 other

**Alignment Scores:**

Pred. No.:	9.7e-58	length:	533
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-801-115B-2 (1-99) x AAA38006 (1-534)

Oy	MetapspsuValGlnProLysIleuYshIstAqProPheCysPheSerValIysGluHis	20
Db	152 ATGATTAAGCTGCAGCCGGAATAATMAACAATCCGCCCTTCTGCTTACGTGTAAAGCCAC	21
Oy	21 ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle	40
Db	212 GTGAGAGATGCTGGCGCTGGATATTATCACTCACTGTAACAACAGTTTCATGCTCATC	27
Oy	41 ValSerValLeuAlaLeuIleProGluThrThrThrIleThrValGlyGlyValPhe	60
Db	272 GTATCTGTGTGGCACTGATACACGAAACCAACACTGACAGTGGTGGAAGGGGTGTTT	33
Oy	61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleIleTyrArgLysLeu	80
Db	332 GCAATTGTGACACAGATGCTGCTGTCCGGACGGGCCCTTATTACCGGAAGCTTCG	39
Oy	81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu	99
Db	392 TTTCATATCCACGCGCTCTTAACGAAAGAAAGCCGTGCAATGAAAGAAAGAAAGTTTG	448

## RESULT 8

AAH98515/c  
ID AAH98515 standard; cDNA; 538 BP

AC AAH98515;

DT 12-OCT-2001 (first entry)

Human EST-derived coding sequence SEQ ID NO: 372

KM Human/sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse  
 KM tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KM diagnostics; forensic test; gene mapping; genetic disorder;  
 KM biodiversity; gene therapy; nutrition; ss.

OS Homo sapiens.

PN W0200154477-A2

PD 02-AUG-2001.

PF 25-JAN-2001; 2001WO-US02687

PR 25-JAN-2000; 2000US-0491404

PR 03-AUG-2000; 2000US-0631451

PR 15-SEP-2000; 2000US-0663870.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

**XX**

DR P-PSDB; AAM23856.

PT Isolated polypeptide

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CC The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
CC of the invention.

Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;

### Alignment Scores:

Pred. No.:	1.01e-57	Length:	538
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-801-115B-2 (1-99) x AAH98515 (1-538)

QY 1 MetAspAsnValGlnInProIlyStIleYshIStaGpProPheCySPheSerValIySGIYHis 20  
 Db 366 ATGGATACAGTCGAGCCGGAATAAACAATACGCCCTTCTGCTTCAGTGTAAAGGCCAC 307  
 QY 21 ValIlySerMetLeuAlaArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40  
 Db 306 GTCAAGATAGCTGGCGCTGATATTATCAACTACACGTAAACACGTTTCATCTCATC 247  
 QY 41 ValSerValLeuAlaLeuIleProGluThrTrpThrIleThrValGIGIYGIYValPhe 60  
 Db 246 GTATCTGTGTGGCACTGATACCAAGAACACAACTTACAGTGGTGGAGGGGTGTT 187  
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyraArgLysLeu 80  
 Db 186 GCATTTGTGACACACAGATGCTGCTTCGGCCGACGGGGCCCTTATTATACGGGAACCTTCG 127  
 QY 81 PheAsnProSerGlyProTyraGlnIlyLysIlySProValHisGlnLysLysGluValLeu 99  
 Db 126 TTTCATATCCAGCGCTCTTACCAAGAAAAGCCGTGcATGAAAAAAGAAAGAGTTTGG 70

## RESULT 5

AAH98548/c  
ID AAH98548 standard; cDNA; 538 BP

AC AAH98548

DT 12-OCT-2001 (first entry)

DE Human EST-derived coding sequence SEQ ID NO: 405.

KM Human, sheep; pig, cow; fruit fly; yeast; hamster; macaque; horse;  
 KM tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KM diagnostics; forensic test; gene mapping; genetic disorder;  
 KM biodiversity; gene therapy; nutrition; ss.

OS Homo sapiens

PN WO200154477-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001; 2001MO-US02687.  
 XX  
 XX 25-JAN-2000; 2000US-0491404.  
 PR 17-JUL-2000; 2000US-0617746.  
 PR 03-AUG-2000; 2000US-0631451.  
 PR 15-SEP-2000; 2000US-0663870.  
 XX  
 (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 XX  
 DR WPI: 2001-476164/51.  
 DR P-PSDB; AAM23889.  
 XX  
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use -  
 XX  
 PS Claim 1; Page 467; 1275pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
 CC of the invention.  
 XX  
 SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1,01e-57 Length: 538  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0  
 US-09-801-115B-2 (1-99) x AAH98548 (1-538)  
 QY 1 MetaspasnaValaGlnProLysIleLysHsArgProPheCysPheSerValLysGlyHis 20  
 DB 366 ATGGATTAACGTCTGACGCCGAAATTAACATCCCTCTGCTTCAAGTGAAGGCCAC 307  
 QY 21 ValLysMetLeuArgLeuAspIleLeaSerLeuValThrThrValPheMetLeuIle 40  
 DB 306 GTGAAGATGCTGCGCTGATATATCAACTACACGTAAACAACAGTATTCATGCTCATC 247  
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuValGlyGlyValPhe 60  
 DB 246 GATATCTGTTGGCTGCTGATACCAAAACCAACATTGACAGTTGGTGAAGGGGTGTT 187  
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80  
 DB 186 GCATCTTGACAGCAGTATGCTGCTTCCGACGGGGCCCTATTATTCGGGAAGCTTCTG 127  
 QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99  
 DB 126 TTCATTCACAGGGGCTCTTACAGAGAAAAAGCGTGCATGAAAAAAGAGTTTGG 70  
 RESULT 10  
 AAH34835  
 ID AAH34835 standard; cDNA, 558 BP.  
 XX  
 AC AAH34835;  
 XX  
 DT 03-SEP-2001 (first entry)  
 XX

DE Human colon cancer antigen encoding cDNA SEQ ID NO:1917.  
 XX  
 KM Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KM colorectal carcinoma; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200122920-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 28-SEP-2000; 2000WO-US26524.  
 XX  
 PR 29-SEP-1999; 99US-0157137.  
 PR 03-NOV-1999; 99US-0163280.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
 PI WPI: 2001-235357/24.  
 DR P-PSDB; AAG75430.  
 DR  
 DR  
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
 PT useful for preventing, diagnosing and/or treating colorectal cancers -  
 XX  
 PS Claim 1; Page 3428; 9803pp; English.  
 XX  
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where  
 CC the proteins are collectively known as colon cancer antigens. The colon  
 CC cancer antigens have cytostatic activity and can be used in gene  
 CC therapy and vaccine production. N and P may be used in the prevention,  
 CC diagnosis and treatment of diseases associated with inappropriate P  
 CC expression. For example, N and P may be used to treat disorders  
 CC associated with decreased expression by rectifying mutations or deletions  
 CC in a patient's genome that affect the activity of P by expressing  
 CC inactive proteins or to supplement the patients own production of P.  
 CC Additionally, N may be used to produce the colon cancer-associated ps,  
 CC by inserting the nucleic acids into a host cell and culturing the cell  
 CC to express the proteins. N and P can be used in the prevention, diagnosis  
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204  
 CC and AAB77789 represent sequences used in the exemplification of the  
 CC present invention.  
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were  
 CC missing at time of publication, meaning no sequences are present for  
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.  
 XX  
 SQ Sequence 558 BP; 150 A; 119 C; 145 G; 141 T; 3 other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1,06e-57 Length: 558  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0  
 US-09-801-115B-2 (1-99) x AAH34835 (1-558)  
 QY 1 MetaspasnaValaGlnProLysIleLysHsArgProPheCysPheSerValLysGlyHis 20  
 DB 147 ATGGATTAACGTCTGACGCCGAAATTAACATCCCTCTGCTTCAAGTGAAGGCCAC 206  
 QY 21 ValLysMetLeuArgLeuAspIleLeaSerLeuValThrThrValPheMetLeuIle 40  
 DB 207 GTGAAGATGCTGCGCTGATATATCAACTACACGTAAACAACATATTCATGCTCATC 266  
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuValGlyGlyValPhe 60  
 DB 267 GATATCTGTTGGCTGCTGATACCAAAACCAACATTGACAGTTGGTGAAGGGGTGTT 326  
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80



PN WO200005367-A2.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 22-JUL-1999; 99WO-JP03929.  
 XX  
 PR 24-JUL-1998; 98JP-0208820.  
 PR 07-AUG-1998; 98JP-0224105.  
 PR 25-AUG-1998; 98JP-0238116.  
 PR 09-SEP-1998; 98JP-0254736.  
 PR 29-SEP-1998; 98JP-0275505.  
 XX  
 PA (SAGA ) SAGAMI CHEM RES CENT.  
 PA (PROT-) PROTEGENE INC.  
 PI Kato S, Kimura T;  
 DR WPI: 2000-182694/16.  
 DR P-PSDB: MAY94861.  
 XX  
 PT Novel human proteins having hydrophobic domains useful for treating  
 PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,  
 PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -  
 XX  
 PS Claim 3; Page 217-218; 351pp; English.  
 XX  
 CC This sequence encodes a human protein of the invention, which has  
 CC hydrophobic domains. The DNA sequences can be used as a probe or as a  
 CC genetic marker. The protein can also be used as a marker, and to identify  
 CC potential genetic disorders. The DNA and protein can also be used as  
 CC nutritional sources or supplements. The protein exhibits cytokine, cell  
 CC proliferation, cell differentiation activities and induces production of  
 CC other stimulating or immune suppressing activity. It can be used in the  
 CC treatment of various immune deficiencies and disorders, and to treat  
 CC infectious diseases caused by viral, bacterial, fungal or other  
 CC infections. The protein is also used for treating autoimmune disorders  
 CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid  
 CC arthritis. It is also useful in the treatment of allergic reactions and  
 CC conditions such as asthma, and in immune suppression after organ  
 CC transplantation. The protein is useful in regulation of haematopoiesis  
 CC and consequently in the treatment of myeloid or lymphoid cell  
 CC deficiencies. It is also used in compositions for tissue growth or  
 CC regeneration. The protein is also used in the treatment of osteoporosis  
 CC or osteoarthritis and in the treatment of periodontal disease and other  
 CC tooth repair processes. The protein is used in the treatment of nervous  
 CC system disorders such as Alzheimer's disease, Parkinson's disease, and  
 CC Huntington's disease. They are useful for protection or regeneration and  
 CC treatment of lung or liver fibrosis, reperfusion injury in various  
 CC tissues, and conditions resulting from systemic cytokine damage. They are  
 CC also used for promoting or inhibiting tissue differentiation. They are  
 CC also used as contraceptives since they exhibit activin or inhibin related  
 CC activities and as a fertility inducing therapeutic. They are used for  
 CC treating various coagulation disorders and in treatment and prevention of  
 CC conditions resulting from coagulation activities e.g. myocardial  
 CC infarction or stroke. They also acts as receptors, receptor ligands or  
 CC inhibitors or agonists of receptor/ligand interactions. They are used to  
 CC treat inflammatory conditions such as septic shock, sepsis, ischaemia  
 CC reperfusion injury, arthritis, and nephritis. They can be used to  
 CC prevent tumours.  
 XX  
 SQ Sequence 297 BP; 81 A; 68 C; 72 G; 76 T; 0 other:

## Alignment Scores:

Pred. No.: 1.52e-57 Length: 297  
 Score: 504.00 Matches: 98  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 98.99% Mismatches: 0  
 Query Match: 99.21% Gaps: 0  
 DB: 21

US-09-801-115B-2 (1-99) x AAA15919 (1-297)

QY 1 MetaspasnyValGlnProlystIleLysHISArgProPheCysPheSerValLysGlyHis 20  
 DB 1 ATGGATTAAGCTGACGCGGAAATATAACATCGCCCTTCTGCTTCAAGTGAAGGCCAC 60  
 QY 21 ValLysMetLeuArgLeuAspIleIleasSerLeuValThrValPheMetLeuIle 40  
 DB 61 GTGAAAGATGCTGGCGGCTGCATATTATCAACTCACTGTAACACACTATTTCATGCTCANC 120  
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
 DB 121 GTATCTGTGTGGCAGTACGATACCAAGCAACCAACCACTTGTGTGGAGGGGTGT 180  
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80  
 DB 181 GCACCTGTGACACAGATAGTCTGTCTGCCGAGGGGCCCTTATTACCGGAAGCTTCG 240  
 QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99  
 DB 241 TTCAATCCGACGCGCTCTTACAGCAAAAGCCGTGCATGAAAAAAGAACTTTTG 297  
 RESULT 13  
 ID AAA15929 standard; cDNA; 467 BP.  
 XX  
 AC AAA15929;  
 XX  
 DT 12-JUN-2000 (first entry)  
 XX  
 DE Human protein clone HP10357 full length coding sequence.  
 XX  
 KW Human protein; hydrophobic domain; nutritional source; haematopoiesis;  
 KW cytokine production; cell proliferation; cell differentiation;  
 KW immune deficiency; infectious disease; autoimmune disorder; asthma;  
 KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;  
 KW allergic reaction; osteoporosis; osteoarthritis; periodontal disease;  
 KW nervous system disorder; Alzheimer's disease; Parkinson's disease;  
 KW Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;  
 KW systemic cytokine damage; tissue differentiation; contraceptive; stroke;  
 KW coagulation disorder; myocardial infarction; inflammatory condition;  
 KW septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;  
 KW nephritis; therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200005367-A2.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 22-JUL-1999; 99WO-JP03929.  
 XX  
 PR 24-JUL-1998; 98JP-0208820.  
 PR 07-AUG-1998; 98JP-0224105.  
 PR 25-AUG-1998; 98JP-0238116.  
 PR 09-SEP-1998; 98JP-0254736.  
 PR 29-SEP-1998; 98JP-0275505.  
 XX  
 PA (SAGA ) SAGAMI CHEM RES CENT.  
 PA (PROT-) PROTEGENE INC.  
 PI Kato S, Kimura T;  
 DR WPI: 2000-182694/16.  
 DR P-PSDB: MAY94861.  
 XX  
 PT Novel human proteins having hydrophobic domains useful for treating  
 PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,  
 PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -  
 XX  
 PS Claim 4; Page 228; 351pp; English.  
 XX  
 CC This sequence encodes a human protein of the invention, which has  
 CC hydrophobic domains. The DNA sequences can be used as a probe or as a  
 CC genetic marker. The protein can also be used as a marker, and to identify





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XX AAA38007;
AC 22-AUG-2000 (first entry)
XX
DE UCK-2 nucleotide sequence.
XX
KM UCK-2; chemotaxis factor; immunocyte; haemopoiesis stimulant; tumour;
XX radiotherapy; chemotherapy; human; ss.
XX
OS Homo sapiens.
XX
PN CN124584-A.
XX
PD 16-FEB-2000.
XX
PF 14-MAY-1999; 99CN-0107284.
XX
PR 14-MAY-1999; 99CN-0107284.
XX
PA (UYBE-) UNIV BEIJING MEDICAL.
XX
PI Ma D, Han W, Zhang Y;
XX
DR WPI; 2000-388170/34.
XX
DR P-PSDB; AAY98143.
XX
PT Chemotactic factor useful for treatment and diagnosis of immunocyte
XX disorders - has immunocyte chemotactic stimulating factor
XX
PS Example 4; Fig 2; 31pp; Chinese.
XX
CC This sequence represents an UCK-2 cDNA sequence encoding a chemotaxis
CC factor polypeptide. The UCK-2 protein exhibits immunocyte chemotaxis
CC activity and a haemopoiesis stimulating effect. The invention relates to
CC UCK proteins, their encoding nucleotide sequences and antibodies and
CC antagonists against the proteins. The nucleotide and protein sequences
CC are useful for the preparation of a composition for the diagnosis and
CC treatment of diseases associated with abnormal immunocyte function and
CC low haemopoiesis function caused by radiotherapy and chemotherapy used to
CC treat tumours and other diseases.
XX
SQ Sequence 459 BP; 123 A; 99 C; 96 G; 141 T; 0 other;
XX
Alignment Scores:
Pred. No.: 5, 43e-53 Length: 459
Score: 471.50 Matches: 99
Percent Similarity: 65.138 Conservative: 0
Best Local Similarity: 65.138 Mismatches: 0
Query Match: 92.81% Indels: 53
DB: 21 Gaps: 1
US-09-801-115b-2 (1-99) x AAA38007 (1-459)
QY 1 MetaSPasnaValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
DB 1 ATGGATAAACGTGACGCGCAAAATAAACAATCGCCCTTCTGCTCAGTGTGAAGGCCAC 60
QY 21 ValLysMetLeuArg----- 25
DB 61 GTGAAGATCTGCGCTGCGCACTAACTGACATCTAGACCTTTTATCATCGCACAA 120
QY 25 ----- 25
DB 121 GCCCCTGAACCATATATTTGTATCATGATTTGAAGTCACCGCTATCTATTTTCATA 180
QY 26 -----LeuAsp 27
DB 181 CTTTATATGTAAGTCACTGATGATTAATGAAGTGTATTTGGCCTTGCTGAT 240
QY 28 IleIleAsnSerLeuValThrValPheMetLeuIleValSerValLeuAlaLeuIle 47
DB 241 ATTATCACTCACTGTGTACACAGTATCATGCTATCAGTATCTGTGTGTGCACTGATA 300

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QY 48 ProGluThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys 67
DB 301 CCAGAAACACACACATTTGACAGTTGTGTGAGGGGTGTTTGTGACACGATATGC 360
QY 68 CysLeuAlaAspGlyAlaLeuIleValArgLysLeuLeuPheAsnProSerGlyProTyr 87
DB 361 TGTCTTGCCGACGGGGCCCTTATTTACGGAGGCTCTGTTCAATCCACAGGCTCTTAC 420
QY 88 GluLysLysProValHisGluLysLysGluValLeu 99
DB 421 CAGAAAAAGCCTGTGATGAAAAAAGAAAGTTTGG 456

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Job time : 217 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 25, 2003, 12:33:06 ; Search time 65 seconds  
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467.092 Million cell updates/sec

Title: US-09-801-115B-2  
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Ygapop 10.0, Ygapext 0.5  
Zgapop 6.0, Zgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Database : Issued Patents.NA:\*

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- 5: /cgn2\_6/ptodata/1/ina/PCrUS.COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	508	100.0	504	4	US-09-149-476-98
2	508	100.0	506	4	US-09-149-476-252
3	357	70.3	392	4	US-09-385-982-95
4	83	16.3	37948	4	US-09-251-645-11
5	73	14.4	1083	4	US-09-116-498-11
6	71	14.0	1083	4	US-09-116-498-11
7	66.5	13.1	720	1	US-08-061-092A-2
8	66	13.0	4403765	4	US-09-103-840A-2
9	66	13.0	4411529	4	US-09-103-840A-1
10	65.5	12.9	43676	3	US-09-356-952-12
11	65	12.8	3872	4	US-09-165-386-1
12	64.5	12.7	1333	1	US-08-684-862-9

13	64.5	12.7	2211	4	US-09-462-844-1	Sequence 1, Appl
14	64.5	12.7	7721	3	US-08-772-270A-14	Sequence 10, Appl
15	64	12.6	17710	4	US-08-976-259-70	Sequence 74, Appl
16	64	12.6	25165	4	US-09-453-702B-39	Sequence 39, Appl
17	63.5	12.5	654	4	US-08-898-416-176	Sequence 176, App
18	63.5	12.5	1785	4	US-09-377-155-8	Sequence 8, Appl
19	63.5	12.5	1785	4	US-09-669-974-8	Sequence 6, Appl
20	63.5	12.5	2153	4	US-09-367-206-6	Sequence 8, Appl
21	63	12.4	1854	1	US-08-249-420-1	Sequence 1, Appl
22	63	12.4	1854	2	US-08-737-663-1	Sequence 1, Appl
23	63	12.4	4403765	4	US-09-103-840A-2	Sequence 2, Appl
24	63	12.4	4411529	4	US-09-103-840A-1	Sequence 1, Appl
25	62.5	12.3	615	4	US-09-134-001C-376	Sequence 376, App
26	62.5	12.3	1105	4	US-09-221-017B-108	Sequence 108, App
27	62.5	12.3	9711	4	US-08-961-527-167	Sequence 167, App
28	62	12.2	745	4	US-09-221-017B-319	Sequence 319, App
29	62	12.2	819	1	US-08-309-182B-2	Sequence 2, Appl
30	62	12.2	6943	4	US-09-453-702B-213	Sequence 213, App
31	61.5	12.1	1327	6	5320941-1	Patent No. 5320941
32	61.5	12.1	1435	2	US-08-878-989-14	Sequence 14, Appl
33	61.5	12.1	1435	4	US-09-272-796-14	Sequence 14, Appl
34	61.5	12.1	3706	4	US-08-913-159-9	Sequence 9, Appl
35	61.5	12.1	3725	1	US-08-155-331-12	Sequence 12, Appl
36	61.5	12.1	3725	1	US-08-424-022-12	Sequence 12, Appl
37	61.5	12.1	3725	2	US-08-424-017B-12	Sequence 12, Appl
38	61.5	12.1	3725	5	PCr-US93-11696-12	Sequence 12, Appl
39	61.5	12.0	1083	4	US-09-116-498-9	Sequence 9, Appl
40	61	12.0	8396	4	US-09-328-174A-1	Sequence 1, Appl
41	61	12.0	8409	4	US-09-167-681-37	Sequence 37, Appl
42	61	12.0	13417	2	US-08-637-739B-37	Sequence 37, Appl
43	61	12.0	13417	3	US-08-871-355A-37	Sequence 37, Appl
44	61	12.0	13417	4	US-09-201-945-37	Sequence 37, Appl
45	61	12.0	61663	4	US-09-453-702B-62	Sequence 62, Appl

## ALIGNMENTS

RESULT 1  
US-09-149-476-98  
Sequence 98, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
EARLIER FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
EARLIER FILING DATE: 1997-05-23

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EARLIER APPLICATION NUMBER: 60/056, 875  
EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048, 964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057, 650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056, 884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057, 669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049, 610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061, 060  
EARLIER FILING DATE: 1997-10-02

## Alignment Scores:

Pred. No.:	2,43e-66	Length:	504
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-801-115b-2 (1-99) x US-09-149-476-98 (1-504)

QY 1 MetaspsnValGlnProLysIleLysHisArgProPheCysPheSerVallySLYHIS 20  
DB 131 ATGGATTAACGCGCAGCGGAAATAAACAATCGCCCTTGCTCATGTGCAAGGCGAC 190  
QY 21 VallySmetLeuAgleuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40  
DB 191 GTGAAGATGCTGCGCGTGATATTATCACTCACTGTACACAGATTCATCATCTCATC 250  
QY 41 ValserValleuAlaIleuIleProGluThrThrIleuThrValIleGlyGlyValPhe 60  
DB 251 GATCTGTGTGGCGCGATGCCAGAACCAACCAATTCGAGTGTGGAGGGGTGTTT 310  
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspIleValLeuIleTyrArgLysLeuLeu 80  
DB 311 GCACCTGTGACAGCAGATATGCTGTGCGCAGGGGCCCTTATTACCGGAACCTCTTG 370  
QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysLysGluValLeu 99  
DB 371 TTCAATCCACGCGGTCTTACAGAAAAAGCCGTGCATGAAAAAAGAAATTG 427

## RESULT 2

US-09-149-476-252

Sequence 252, Application US/09149476

Patent No. 6420526

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERENCE: P2002P1

CURRENT APPLICATION NUMBER: US/09/149, 476

EARLIER FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: PCT/US98/04493

EARLIER FILING DATE: 1998-03-06

EARLIER APPLICATION NUMBER: 60/040, 162

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040, 333

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/038, 621

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040, 626

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040, 334

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040, 336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040, 163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047, 600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 503  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 592  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 581  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 584  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 500  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 587  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 492  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 582  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 596  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 612  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 632  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 601  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043, 580  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 568  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 314  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 569  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 311  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 671  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 674  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 669  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 312  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 313  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 672  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043, 315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048, 974

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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11

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; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Alignment Scores:
Pred. No.: 2,44e-66 Length: 506
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

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US-09-801-115b-2 (1-99) x US-09-149-476-252 (1-506)
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Qy 1 MetaspasnaValGlnPolysilleyshisArgProheCysPheSerVallysglyHs 20
Db 117 ATGGATACGTCGCGCGGAAATAAACATCGCCCTTCTGCTTCAGTGAAAGGCCAC 176
Qy 21 VallysmetLeuArgLeuAspIleIleasnSerLeuValThrValPheMetLeuIle 40
Db 177 GTGAAGATGTCGCGCGGATATTAACAATCACTGCTGTAACAACAATATTCATGCTCATC 236
Qy 41 ValSerValLeuAlaLeuIleProGluThrThrLeuThrValAlaIleGlyValPhe 60
Db 237 GTATCTGTGTTCGACATGATACCAAGAACCAATTCACACTGTGTGAGGGGTGTT 296
Qy 61 AlaleuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleThrArgIleLeu 80
Db 297 GCACCTGTGACAGCAGATGCTGCTTGGACGAGGGGCCCTTATTAACGGAAGCTTCG 356
Qy 81 PheasnProSerGlyProIleGlnIleValIleValIleGluIleValIleValIle 99
Db 357 TTCAATCCACGGGCTCTTACCAAGAAAGCCGTGCTCATGAAGAAAAAGAACTTTTG 413

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RESULT 3
US-09-385-982-95
; Sequence 95, Application us/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS: II

```

FILE REFERENCE: CCDA-260X  
CURRENT APPLICATION NUMBER: US/09/385,982  
EARLIER FILING DATE: 1999-08-30  
EARLIER APPLICATION NUMBER: 09/328,111  
EARLIER FILING DATE: 1999-06-08  
EARLIER APPLICATION NUMBER: 60/117,393  
EARLIER FILING DATE: 1999-01-27  
EARLIER APPLICATION NUMBER: 60/098,639  
EARLIER FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 544  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 95  
LENGTH: 392  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: (1)...(392)  
OTHER INFORMATION: n = A,T,C or G  
US-09-385-982-95

Alignment Scores:  
Pred. No.: 4.43e-44 Length: 392  
Score: 357.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 70.28% Indels: 0  
DB: 4 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-385-982-95 (1-392)

QY 26 LeuaspilleleasenseleuValThrThrValPheMetLeuileValSerValleuila 45  
|||||  
DB 44 CTGTGATTATTAATCTCACTGTGTACACAGATTCAAGCTCATGTCGTGTGCA 103  
|||||

QY 46 LeuileProgluThrThrThrleuThrValGlyGlyGlyValPheAlaLeuValThra 65  
|||||  
DB 104 CTGATACCAAGAAACCAACATTTGACAGTGTGTGAGGGGTGTTCACATTGTGACACCA 163  
|||||

QY 66 ValCysCysLeuAlaAspGlyAlaLeuileTyraArgysleuLeuPheAsnProserly 85  
|||||  
DB 164 GTATCGTGTCTTGGCGAGGGGCGCTTATTACCGGAAGCTTGTTCATCCACGGCT 223  
|||||

QY 86 ProTyGlnTyLeysProValHISGluTyls 96  
|||||  
DB 224 CCTTACCAAGAAACCGCTGTGATGAAAAA 256  
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RESULT 4  
US-09-251-645-11  
Sequence 11, Application US/09251645  
Patent No. 6281413  
GENERAL INFORMATION:  
APPLICANT: Kramer, Vance C.  
APPLICANT: Morgan, Michael K.  
APPLICANT: Anderson, Arne R.  
APPLICANT: Hart, Hope  
APPLICANT: Warren, Gregory W.  
APPLICANT: Dunn, Martha  
APPLICANT: Chen, Jeng S.  
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS  
TITLE OF INVENTION: AND NUCLEIC ACID SEQUENCES CODING THEREFOR  
FILE REFERENCE: CGC1963/A  
CURRENT APPLICATION NUMBER: US/09/251,645  
CURRENT FILING DATE: 1999-02-17  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 11  
LENGTH: 37948  
TYPE: DNA  
ORGANISM: Photorhabdus luminescens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (15171)..(18035)

OTHER INFORMATION: orf5  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (23766)..(31336)  
OTHER INFORMATION: hph2  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (31393)..(35838)  
OTHER INFORMATION: orf2  
US-09-251-645-11

Alignment Scores:  
Pred. No.: 1.93 Length: 37948  
Score: 83.00 Matches: 28  
Percent Similarity: 51.76% Conservative: 16  
Best Local Similarity: 32.94% Mismatches: 21  
Query Match: 16.34% Indels: 20  
DB: 4 Gaps: 5

US-09-801-115B-2 (1-99) x US-09-251-645-11 (1-37948)

QY 12 ProphecysPheSerVallyGlyHisVallyMetLeuArgleuAspilleleasense 31  
||| |||  
DB 6476 CCAATATGCTTCTTAAGGAATGACACCTGAATAATCAACAACTTAACCTTAATACAGT 6535  
||| |||

QY 32 LeuValThrThrValPheMetLeuileValSerValleuAlaLeuileProgluThrThr 51  
||| |||  
DB 6536 TTGATTA-----CTAATAGTATTAATGTCATATATCGCTATGCAAGAGCTACGAA 6589  
||| |||

QY 52 Thrleu-----ThrValGlyGlyGlyValPheAlaLeuValThra 65  
||| |||  
DB 6590 TCCCTTCATCAGTAATAGTAATAGTAATACGCTTATGTTGGGAGATGGCTATC-----TGA 6643  
||| |||

QY 66 ValCysCysLeuAlaAspGlyAlaLeuileTyraArgysleuLeuPheAsnProser--- 84  
||| |||  
DB 6644 GTATGCTGTATGCGCGAA-----ATATTTCAGCCATCAAC 6679  
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QY 85 ---GlyProTyGln 88  
||| |||  
DB 6680 TGAAGTCCTCATCAG 6694  
||| |||

RESULT 5  
US-09-116-498-11  
Sequence 11, Application US/09116498  
Patent No. 6251582  
GENERAL INFORMATION:  
APPLICANT: Littman, Dan R.  
APPLICANT: Deng, Hongkui  
APPLICANT: Unutmaz, Derya  
APPLICANT: Ramani, Vineet N.K.  
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS  
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF  
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USE  
THEREOF  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESS: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/116,498  
FILING DATE: 16-Jul-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1049-1-009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1083 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Piftail macaque  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-116-498-11

Alignment Scores:  
Pred. No.: 0.3 Length: 1083  
Score: 73.00 Matches: 25  
Percent Similarity: 39.33% Conservative: 10  
Best Local Similarity: 28.09% Mismatches: 24  
Query Match: 14.37% Indels: 30  
DB: 4 Gaps: 4

US-09-801-115B-2 (1-99) x US-09-116-498-11 (1-1083)

QY 8 ILEYSHSARGPROPHCYSPHESERVALLYSGLYHSVALLYSMETLEUAARGLEUASP 27  
DB 529 ATTGATGATAGAGCCATCTGT-----GCAGAGAAAGGCGACCTCCACTTAAA 576  
QY 28 ILEIENSERLEUVALTHRVAlpheMetLeuLeuValSerValLeuAlaLeuIle 47  
DB 577 CTCATATGGTCCCTGGCGCTTAATTTCACCTTTTGTCCCTTGTG-----627  
QY 48 PROGLUTHRTHRLTHLEUTHRVAlGlyGlyValPheAlaLeuValThAlaValCys 67  
DB 628 -----AGCATTTGACCTGCTACTGT 648  
QY 68 CYSLEUALASPGLYALALEUILETYRARGLYSLEUleuPheAsnProSerGlyProTyr 87  
DB 649 TGCATTGCA-----AGGAAGCTGTGTGCCCAT-----TAC 678  
QY 88 GLNLYSLSPROVALHISGLULYSLYS 96  
DB 679 CAGCAGTCAGGAAAGCACACAAAAG 705

## RESULT 6

US-09-116-498-7  
Sequence 7, Application US/09116498  
Patent No. 6251582  
GENERAL INFORMATION:  
APPLICANT: Littman, Dan R.  
Inventor: Deng, Hongkui  
Ramani, Vineet N.K.  
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS  
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF  
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES  
THEREOF  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/116,498  
FILING DATE: 16-Jul-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1049-1-009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1083 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-116-498-7

Alignment Scores:  
Pred. No.: 0.594 Length: 1083  
Score: 71.00 Matches: 24  
Percent Similarity: 39.33% Conservative: 11  
Best Local Similarity: 26.97% Mismatches: 24  
Query Match: 13.98% Indels: 30  
DB: 4 Gaps: 4

US-09-801-115B-2 (1-99) x US-09-116-498-7 (1-1083)

QY 8 ILEYSHSARGPROPHCYSPHESERVALLYSGLYHSVALLYSMETLEUAARGLEUASP 27  
DB 529 ATTGATGATAGAGCCATCTGT-----GCAGAGAAAGGCGACCTCCACTTAAA 576  
QY 28 ILEIENSERLEUVALTHRVAlpheMetLeuLeuValSerValLeuAlaLeuIle 47  
DB 577 CTCATATGGTCCCTGGCGCTTAATTTCACCTTTTGTCCCTTGTG-----627  
QY 48 PROGLUTHRTHRLTHLEUTHRVAlGlyGlyValPheAlaLeuValThAlaValCys 67  
DB 628 -----AGCATTTGACCTGCTACTGT 648  
QY 68 CYSLEUALASPGLYALALEUILETYRARGLYSLEUleuPheAsnProSerGlyProTyr 87  
DB 649 TGCATTGCA-----AGGAAGCTGTGTGCCCAT-----TAC 678  
QY 88 GLNLYSLSPROVALHISGLULYSLYS 96  
DB 679 CAGCAGTCAGGAAAGCACACAAAAG 705

## RESULT 7

US-08-061-092A-2/c  
Sequence 2, Application US/08061092A  
Patent No. 5587458  
GENERAL INFORMATION:  
APPLICANT: KING, C R  
APPLICANT: KASPRZYK, Philip G  
APPLICANT: BIRD, Robert E  
TITLE OF INVENTION: ANTI-erbB-2 ANTIBODIES, COMBINATIONS  
THEREOF, AND THERAPEUTIC AND DIAGNOSTIC USES THEREOF  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: George Mason Bldg., Washington & Prince Sts.  
CITY: Alexandria  
STATE: Virginia





```

Db      1498059 CTGGAGCAGACGAGACACCAATCGCGTCCGGGTGCTGCCGCTATCG 1498000
      28 lleleasrleuValThrValPheMetleuIleValSerValleuAlaLeuIle 47
Db      1497999 GTGGCCGAGCTGTGCGCCACCGAGGTGTGCCCGTCGACACGCGTATGACC----- 1497946
      48 ProgluThrThrLeuThrValGlyGlyValAlaPheAlaLeuValThrAlaValGly 67
Db      1497945 -----TGGGCAACGCTGACATCGCGGGTGTGACGCGATGCGCAGCATGGGCG 1497892
      68 CysleuAlaAspGlyAlaLeuIleTyrArgIysleuLeuPheAsnProSerGlyProTyr 87
Db      1497891 CTGACTGCAGACACCGCC-----TGGCGTGGCGCTG-----GACGTGGCGCTCGCCTTTC 1497844
      88 GluIysLysProValHisGluLysLysGluValleu 99
Db      1497843 CAG-----CAGCCAAAGTCGGGAATCTC 1497820

RESULT 10
US-09-356-952-12/C
; Sequence 12, Application US/09356952
; Patent No. 6117663
; GENERAL INFORMATION:
; APPLICANT: Borjacks-Stodin, Ann
; APPLICANT: Margalit, S. M.
; APPLICANT: Bor-Sogil, Dafna
; APPLICANT: Cole, Philip
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 600-1-228H
; CURRENT APPLICATION NUMBER: US/09/356,952
; CURRENT FILING DATE: 1999-07-19
; EARLIER APPLICATION NUMBER: 60/093,631
; EARLIER FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 43676
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-356-952-12

Alignment Scores:
Pred. No.: 943          Length: 43676
Score: 65.50           Matches: 26
Percent Similarity: 44.87% Conservative: 9
Best Local Similarity: 33.33% Mismatches: 32
Query Match: 12.89%     Indels: 11
                        Gaps: 3

US-09-801-115b-2 (1-99) x US-09-356-952-12 (1-43676)
QY      33 ValThrThrValPheMetleuIleValSerValleuAlaLeuIleProgluThrThr 52
      43598 GTCCGTAAAGCGCTTGTCTTATCGTGAAGCATCTCTCACTTATTCGAATTAACAATAT 43539
QY      53 leuThrValGly-----GlyGlyValPheAlaLeuValThrAla 65
      43538 ATGAAAGTTAATGATTTGTCCAAATTCGTCGATGAGGCGTTTACCGCGCATTACTTAT 43479
QY      66 ValCysCysleuAlaAspGlyAlaLeuIleTyrArgIysleu---leuPheAsnProSer 84
      43478 ATCTGCTTATCATCAGCATCATGATTAATTCGTAAGGTTGCGTGCACCATCTG 43419
QY      85 GlyProTyrGluLysLysPro-----ValHisGluLysLysGluValleu 99
      43418 AATAAGCAATATATAAACCATCATGTTAAGCTTTTACCAAAAGCAGAACTCTG 43365

RESULT 11
US-09-165-396-1
; Sequence 1, Application US/09165396

```

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; Patent No. 6441134
; GENERAL INFORMATION:
; APPLICANT: BECKER, JEFFREY W.
; APPLICANT: LUBKOWITZ, MARK A.
; TITLE OF INVENTION: ISOLATED CANDIDA ALBICANS OLIGOPEPTIDE TRANSPORTER GENE
; FILE REFERENCE: 372,6520P
; CURRENT APPLICATION NUMBER: US/09/165,396
; CURRENT FILING DATE: 1998-10-02
; EARLIER APPLICATION NUMBER: PCT/US98/02332
; EARLIER FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: 60/037,859
; EARLIER FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3872
; TYPE: DNA
; ORGANISM: C. albicans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (481..2106, 2165..2887)
US-09-165-396-1

Alignment Scores:
Pred. No.: 30.7          Length: 3872
Score: 65.00           Matches: 16
Percent Similarity: 55.32% Conservative: 10
Best Local Similarity: 34.04% Mismatches: 21
Query Match: 12.80%     Indels: 0
                        Gaps: 0

US-09-801-115b-2 (1-99) x US-09-165-396-1 (1-3872)
QY      32 leuValThrThrValPheMetleuIleValSerValleuAlaLeuIleProgluThrThr 51
      1876 CTAGTGTCTCTCTGCTCTTTTTCGTTATGTCATAGCCACCGTAGCTGCGCTACT 1935
QY      52 ThrLeuThrValGlyGlyGlyValPheAlaLeuValThrAlaValCysCysleuAlaAsp 71
      1936 GAATGCCAGTATGAGGGGTTTATTTTGTCTTATCATCAGCATATATTTTATTAACCC 1995
Db      72 GlyAlaLeuIleTyrArgLys 78
      1996 GTTGCATCATTTATGCANAA 2016

RESULT 12
US-08-684-862-9/C
; Sequence 9, Application US/08684862
; Patent No. 5759541
; GENERAL INFORMATION:
; APPLICANT: Bach, Alfred
; APPLICANT: Hilleu, Heinz
; APPLICANT: Bialojan, Siegfried
; TITLE OF INVENTION: No. 5759541el Proteins, the Preparation and Use
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kell & Weinkauff
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage
; COMPUTER: IBM AT-compatible, 80286 processor
; OPERATING SYSTEM: MS-DOS version 5.0
; SOFTWARE: WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,862
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: US/08/361,705  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/966,040  
FILING DATE: 30-DEC-1992  
APPLICATION NUMBER: PCT/EP91/01361  
FILING DATE: 19-JUL-1991  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1333 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: Agkistrodon rhodostoma  
FEATURE:  
LOCATION: 231 to 935  
OTHER INFORMATION: the coding region shown in (2)(1x)(B)  
OTHER INFORMATION: codes for the protein of SEQ ID NO: 4  
US-08-684-862-9

Alignment Scores:  
Pred. No.: 7.47 Length: 1333  
Score: 64.50 Matches: 19  
Percent Similarity: 50.00% Conservative: 9  
Best Local Similarity: 33.93% Mismatches: 19  
Query Match: 12.70% Indels: 9  
DB: 1 Gaps: 2

US-09-801-115B-2 (1-99) x US-08-684-862-9 (1-1333)

OY 39 LeuileValSerValleuAlaLeuileProgluThrThrleuThrValGlyGly 58  
DB 1295 CTATATATCTCTCTCTCTCGAGTCTCTCAGTCTTACAGTCTTATTCGAATCT 1236  
OY 59 ValpheAlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyArgLys 78  
DB 1235 GTTTCCTGCTCAGATTGATTGCTGCTAGGAT-----AAG 1194  
OY 79 LeuLeuPheAsnProSerGlyProTyGlnLysProValHisGlu 94  
DB 1193 TTGTTTTCGAATCTCTGATTTTC-----CCCCCCCAAG 1155

RESULT 13  
US-09-462-844-1  
Sequence 1, Application US/09462844  
Patent No. 6258563  
GENERAL INFORMATION:  
APPLICANT: Quax, Wilhelmus J.  
TITLE OF INVENTION: Increasing Production of Proteins in  
FILE REFERENCE: Gram-Positive Microorganisms  
CURRENT APPLICATION NUMBER: US/09/462,844  
CURRENT FILING DATE: 2000-01-13  
PRIOR APPLICATION NUMBER: PCT/US98/14786  
PRIOR FILING DATE: 1998-07-15  
PRIOR APPLICATION NUMBER: EP 97305286.3  
PRIOR FILING DATE: 1997-07-16  
PRIOR APPLICATION NUMBER: EP 97305344.0  
PRIOR FILING DATE: 1997-07-17  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 2211  
TYPE: DNA  
ORGANISM: Bacillus subtilis  
US-09-462-844-1

Alignment Scores:  
Pred. No.: 15.8 Length: 2211  
Score: 64.50 Matches: 13  
Percent Similarity: 44.09% Conservative: 18

Best Local Similarity: 30.11% Mismatches: 29  
Query Match: 12.70% Indels: 24  
DB: 4 Gaps: 3

US-09-801-115B-2 (1-99) x US-09-462-844-1 (1-2211)

OY 16 SerValLysGlyHisValLysMetLeuArgLeuAspIleLeuSerLeuValThrThr 35  
DB 1132 TCTGTAAAGGGTTTCGACATGCGATCGATCTTTCATTTTGACAGCTTATCACTGCC 1191  
OY 36 ValPheMetLeuIleValSerValLeuAlaLeuIleProgluThrThrleuThrVal 55  
DB 1192 GTTTCCTGCTCAGATTGATTGCTGCTAGGAT-----AAG 1248  
OY 56 GlyGlyGlyValPheAlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIle 75  
DB 1249 AAAAAGGCTGCTTGTCT-----GTC 1269  
OY 76 TyrArgLysLeuLeuPheAsn-----ProSerGlyPro 86  
DB 1270 AATAGAAACATATTCATGATATTCAGATGAGTAAATACAGAGCCGATACGCCA 1329  
OY 87 TyrGlnLysLysProValHisGluLysLysGluValLeu 99  
DB 1330 TTCCAAAATG-AGATTTCACGAGCAACGAATATCTT 1367

RESULT 14  
US-08-772-270A-14/c

Sequence 14, Application US/08772270A

Patent No. 6019984

GENERAL INFORMATION:

APPLICANT: MacInnes, Janet

APPLICANT: Ricciardi, Paul

APPLICANT: Mallard, Bonnie

APPLICANT: Rosendal, Soren

TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR

TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bereskin & Parr

STREET: 40 King Street West

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5H 3Y2

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/772,270A

FILING DATE: December 23, 1996

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Gravalle, Michelle

REGISTRATION NUMBER: 40,261

REFERENCE/DOCKET NUMBER: 6580-81

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 364-7311

TELEFAX: (416) 361-1398

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 7721 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORGANISM: Actinobacillus pleuropneumoniae

US-08-772-270A-14

Alignment Scores:

Pred. No.: 101  
 Score: 64.50  
 Percent Similarity: 39.60%  
 Best Local Similarity: 22.77%  
 Query Match: 12.70%  
 DB: 3  
 Gaps: 4

US-09-801-115B-2 (1-99) x US-08-772-270A-14 (1-7721)

QY 22 LysMetLeuArgLeuAspIleIleAsnSer-----LeuValThr 34  
 DB 7519 CGTCTCTAGACTTCACTAATAGATCTCTAATGACGACGATGAGAACTGATTAACA 7460  
 QY 35 ThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 52  
 DB 7459 CCGCGTTCTCCGTTTATTTCTGCAATACGCGCATTTCCGAAACCTAATGATTTCT 7400  
 QY 53 LeuThrValGlyGlyValPheAlaLeuValThrAlaVal----- 66  
 DB 7399 TATACACATCTGTAAATGTTTTCTGTAAATCTCAATATGAAATGAAATGAACTAAACCA 7340  
 QY 67 -----CysCysLeuAlaAspGlyAlaLeuIleTyrArg----- 77  
 DB 7339 AGCTGAGGTGCTCAATACATCAAGAGTAATAGTTTACTTTCCATAGAGATAACCA 7280  
 QY 78 -----LysLeuLeuPheAsnProSerGlyProTyrGlnLys 90  
 DB 7279 TATCTTGTAGGAAAGTTTCCACTTAATATGCTCTCTGTCATATTCAACAA 7220  
 QY 91 Pro 91  
 DB 7219 CCA 7217

# RESULT 15

US-08-976-259-70  
 ; Sequence 70, Application US/08976259  
 ; Patent No. 6316609

GENERAL INFORMATION:

APPLICANT: Dillon, Patrick J.

APPLICANT: Choi, Gil H.

APPLICANT: Welch, Rodney A.

TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli

Patent No. 6316609

NUMBER OF SEQUENCES: 142

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Ave, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/976,259

FILING DATE: Herewith

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/031,626 AND US 60/061,953

ATTORNEY/AGENT INFORMATION:

NAME: Steife, Eric K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0740002/EKS/CBM

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 17710 base pairs

TYPE: nucleic acid

STRANDEDNESS: double  
 TOPOLOGY: linear  
 US-08-976-259-70

Alignment Scores:

Pred. No.: 412

Score: 64.00

Percent Similarity: 44.00%

Best Local Similarity: 25.00%

Query Match: 12.60%

DB: 4

Gaps: 3

Length: 17710

Matches: 25

Conservative: 19

Mismatches: 40

Indels: 16

US-09-801-115B-2 (1-99) x US-08-976-259-70 (1-17710)

QY 4 ValGlnProLysIleLysHisArgProPheCysPheSerVal----- 17  
 DB 17166 GTTCAGGGTATGCTGAAGCATATGATTTTTCAGCGCCGACGCTGCGGACGGG 17225  
 QY 18 -----LysGlyHisValLysMetLeuArgLeuAspIleIleAsnSer 31  
 DB 17226 CTCAGAAAGGAGCGGCTGCAGGAAATATCAGTGCCTGAACAAAGTATGAAGGGGTG 17285  
 QY 32 LeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 51  
 DB 17286 CTGGTACATCTCTGCGACTGGTAGCTGTACACACGCGCCCTGACATGATCAAAATGTG 17345  
 QY 52 ThrLeuThrValGlyGlyValPheAla-----LeuValThrAlaValCysCysLeu 69  
 DB 17346 CGGGAGGAGATCTCGGTGGCGAGTTTCATGAGAAATTTCCCGTGGCATCTCTGTG 17405  
 QY 70 AlaAspGlyAlaLeu-----IleTyrArgLysLeuLeuPheAsnProSerGlyProTyr 87  
 DB 17406 GCAGGTGTGTCTGCGGGTCAATGCGCGGGGATATGTTTCACTGACGACCATTT 17465

Search completed: June 25, 2003, 13:33:51

Job time : 1226 secs



US-09-801-115B-2 (1-99) x US-09-918-995-6534 (1-422)

QY	1	MeLAspAsuValGIProVysILeYshsAtgProPhcYsPheSeValYsGLVhIs	20
Db	31	ATGAGTAAGCTGACGCCAAATTAACAATGCCCTTCCTTCACGTGTAAGGCCAC	90
QY	21	ValYsMetLeuAArgLeuAspILeIleAsnSerLeuValYThrThValPheMetLeuIle	40
Db	91	GTGAACATCTCGCGCTGATTTATCACTCACCTGGTAACAAAGATTAATCTCATC	150
QY	41	ValSerValLeuAlaLeuIleProGIunThrThrLeuThrArgLsGLYGLVValPhe	60
Db	151	GTATCTGCTTGGCACTGATACCAAAACCAACATTTGACAGTTGGTAGAGGGGT	210
QY	61	AlaLeuValThrAlaValAlcYsCysLeuAlaAspGlyAlaLeuIleYrArgLysLeuLeu	80
Db	211	GCCTGTGTACAGCAGTATGCTCTTCCACAGCGGGCCCTTATTTACCGGAACCTTCTG	270
QY	81	PheAsnProSerGlyProThrGlnLysLysProValHsGlnLysLysGlnValLeu	99
Db	271	TTTCATCCACGGCGCTCTTACAGAAAGAGCTGTGCATGAAAGAAAGAAAGAGTTTG	327

## RESULT 2

```

? Sequence 397, Application US/09822846
? Publication No. US20030027139A1
? GENERAL INFORMATION:
? APPLICANT: Jacobs, Kenneth
? APPLICANT: McCoy, John M.
? APPLICANT: Lavallie, Edward R.
? APPLICANT: Collins-Racie, Lisa A.
? APPLICANT: Evans, Cheryl
? APPLICANT: Merberg, David
? APPLICANT: Tracy, Maurice
? APPLICANT: Agostino, Michael J.
? APPLICANT: Steininger II, Robert J.
? APPLICANT: Bowman, Michael R.
? APPLICANT: Spaulding, Yikkl
? APPLICANT: Wong, Gordon G.
? APPLICANT: Clark, Hilary
? APPLICANT: Pechtel, Kim
? APPLICANT: Howes, Steven H.
? APPLICANT: Resnick, Richard J.
? APPLICANT: Gulukota, Kamalakhar
? APPLICANT: Graham, James R.
? APPLICANT: Genetics Institute, Inc.
? TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
? FILE REFERENCE: GIN 6400
? CURRENT APPLICATION NUMBER: US/09/822,846
? CURRENT FILING DATE: 2001-03-29
? PRIOR APPLICATION NUMBER: 60/195,605
? PRIOR FILING DATE: 2000-04-06
? NUMBER OF SEQ ID NOS: 629
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 397
? LENGTH: 439
? TYPE: DNA
? ORGANISM: Homo sapiens
?-S-09-822-846-397

```

Pred. No.:	1,14e-63	Length:	439
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-801-115B-2 (1-99) x US-09-822-846-397 (1-439)

QY. 1 MetaspasnaValGlnProLysStIeLysHisArgProPhocysPheSerValLysGlyHis 20  
|||||

Db	81	ATGGATTAACGTCAGCGCAAGAAATAAACAATGCGCCCTTCTGCTCACTGTGAAGGGCCAC	140
Qy	21	ValIysMetLeuArgIeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle	40
Db	141	GTTAAAGATCTCTCGCGTGATATTTATTCACACTCACTCGTAAACAAGATTTCATGCTCATC	200
Qy	41	ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValLGIyGIyValPhe	60
Db	201	GTATCTGCTTGCGCACTGATACCAAAACCAACACATTGACAGTTGGTGGAGGGGCTGTTT	260
Qy	61	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu	80
Db	261	GCACCTGTACACGCAAGTATGCTGTCTTCCACACGGGGCCCTTATTTACCGAAGCTTCTG	320
Qy	81	PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysLysGluValLeu	99
Db	321	TTCAAATCCAGGGGCTCTTACCAAGAAAAAGCTGTGCATGAAAAAAGAAAGTTTTC	377

### RESULT 3

```

: Sequence 98, Application US/09809391
: Publication No. US20030049618A1
: GENERAL INFORMATION:
: APPLICANT: Ruben et al.
: TITLE OF INVENTION: 186 Human Secreted proteins
: FILE REFERENCE: P2002P2
: CURRENT APPLICATION NUMBER: US/09/809,391
: CURRENT FILING DATE: 2001-03-16
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 761
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 98
: LENGTH: 504
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-809-391-98

```

Alignment Scores:	
Pred. No.:	1,39e-63
Score:	508.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	9
Length:	504
Matches:	99
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-801-115B-2 (1-99) X US-09-809-391-98 (1-504)

QY	1	MeAspAsnValGILProCysIIElyshIstqPhePheCysPheSerValIysGILHis	20
Db	131	ATGGATAAAGCTGCACCCGAAATATAACATGCGCCCTTCCTCCTCAGCTGTAAGGCCAC	190
QY	21	ValIysMetLeuArgLeuAspIIEIleAsnSerLeuValIThrThrValPheMetLeuIle	40
Db	191	GTGAAGATCTCTCGGCTGGATATTATTCACATCAGCTGGTAACACAGTATTCATGCTCATC	250
QY	41	ValSerValIleuAlaIleuIleProGIuThrThrThrIleThrValIglYglYValPhe	60
Db	251	GNATCTGTTTGGCACTGATACCGAATAACCAACATTGACAGTTGGTGGAGGGGTTTT	310
QY	61	AlaLeuValThrAlaValAlaCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu	80
Db	311	GCACCTGTGCAGCGAGTATGCTGTCCTTCCACAGCGGGCGCCCTTATTATTCGCGGAAGCTTCTG	370
QY	81	PheAsnProSerGIuProTyrGIuIuLysProValHisGIuLysLysGIuValIleu	99
Db	371	TTTCATATCCAGGGGGTCTTACCGAATAAGGCTTGATGTAATAAAAAAGAGATTTTG	427

## RESULT 4

```

US-09-809-391-252
; Sequence 252, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.

```

Pred. No.:	1,52e-63	Length:	534
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-801-115B-2 (1-99) x US-09-801-115-1 (1-534)

QY	1	MetAspAsnValAlaGlnProLysIleLysHisArgProPheCysPheSerValLysGLYHis	20
Db	152	ATGGATACGGTCGACGGCGAAATTAACAATGACCGCCCTTCGCTTCACGTGGAAGGCCAC	211
QY	21	ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThraValPheMetLeuIle	40
Db	212	GTGAAGATGCTCGCGGCTGGATATATATACACTCACTGTTAACACAGATATCATGCTCATC	271
QY	41	ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValAlaGlyGlyValPhe	60
Db	272	GTATCTGTGGTCACATGATACAGAAACCAACAATGACAGTGGTGAAGGGGTGTTT	331
QY	61	AlaLeuValThrAlaValCysCysAlaLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu	80
Db	332	GCACTTGTGACGACGAGATGCTGCTTCGCCACGGGGCCCTTATTACGGAGCTCTG	391
QY	81	PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysLysGluValLeu	99
Db	392	TTCATCCCAACGGGTCCTTACCAGAAAAGCCTGTGATGAAAAAAGAAAGTTTG	448

RESULT 6

US-10-106-698-1927

; Sequence 1927, Application US/10106698

; Publication No. US20030109690A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides

; FILE REFERENCE: PA005P1

; CURRENT APPLICATION NUMBER: US/10/106,698

; CURRENT FILING DATE: 2002-03-27

; PRIOR APPLICATION NUMBER: PCT/US00/26524

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US 60/157,137

; PRIOR FILING DATE: 1999-09-29

; PRIOR APPLICATION NUMBER: US 60/163,280

; PRIOR FILING DATE: 1999-11-03

; NUMBER OF SEQ ID NOS: 8564

; SOFTWARE: PatentIn Ver. 3.0

; SEQ ID NO 1927

; LENGTH: 558

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (514)..(514)

; OTHER INFORMATION: n equals a,t,g, or c

US-10-106-698-1927

Alignment Scores:

Pred. No.:	1,62e-63	Length:	558
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-801-115B-2 (1-99) x US-10-106-698-1927 (1-558)

QY	1	MetAspAsnValAlaGlnProLysIleLysHisArgProPheCysPheSerValLysGLYHis	20
Db	147	ATGGATTAAGTCGACCGCGAAATTAACAATCATGCCCTTCCTTCAGTGTGAAGGCCAC	206
QY	21	ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThraValPheMetLeuIle	40

Db 207 GTGAGATGCTGGCGCTGATATATATCACTGATGTAACAAGATATTATTCATGCTCATC 266  
Qy 41 ValSerValLeuAlaLeuIleProGluThrThrLeuThValGlyGlyAlaPhe 60  
Db 267 GTATCTGTGTGGCACTGATACCAAGAACCAACCTTACAGTTGGAGGGGTGTT 326  
Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80  
Db 327 GCACCTGTGACAGCATGATGCTGTCTGGCAGCGGGCCCTTATTACCGAAGCTTCG 386  
Qy 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99  
Db 387 TTCATGCCAGCGGTCTTACCAAGAAAGCCTGTGCATGAAAGAAAGATTG 443

RESULT 7  
US-09-918-995-19489  
; Sequence 19489, Application US/09918995  
; Publication No. US2003007363A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; LENGTH: 512  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)...(512)  
; OTHER INFORMATION: n - A,T,C or G  
US-09-918-995-19489

Alignment Scores:  
Pred. No.: 1,04e-62 Length: 512  
Score: 502.00 Matches: 98  
Percent Similarity: 98.99% Conservative: 0  
Best Local Similarity: 98.99% Mismatches: 1  
Query Match: 98.82% Indels: 0  
DB: Gaps: 0

US-09-801-115b-2 (1-99) x US-09-918-995-19489 (1-512)

Qy 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20  
Db 142 ATGGATTACGTGCAGCCGCAAAATATAACATGCGCCCTTCTGCTTCAAGTGAAGGCCAC 201  
Qy 21 ValLysMetLeuAlaGlyLeuAspIleIleAsnSerLeuValThrThrAlaPheMetLeu 40  
Db 202 GTGAAGAGTGTGGCGCTGATATATATCACTGATGTAACAACAGATTCATCTCTATC 261  
Qy 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThValGlyGlyAlaPhe 60  
Db 262 GTATCTGTGTGGCACTGATACCAAGAACCAACATTCAGATTGGTGGAGGGGTGTT 321  
Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80  
Db 322 GCACCTGTGACAGCATGATGCTGTCTGGCAGCGGGCCCTTATTACCGAAGCTTCG 381  
Qy 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99  
Db 382 TTCATGCCAGCGGTCTTACCAAGAAAGCCTGTGCATGAAAGAAAGATTG 438

RESULT 8  
US-09-801-115-3  
; Sequence 3, Application US/09801115  
; Patent No. US20020001828A1

; GENERAL INFORMATION:  
; APPLICANT: Ma, D.  
; APPLICANT: Han, W.  
; APPLICANT: Zhang, Y.  
; APPLICANT: Song, Q.  
; APPLICANT: Di, C.  
; APPLICANT: Huang, J.  
; APPLICANT: Tang, J.  
; APPLICANT: Chen, G.  
; TITLE OF INVENTION: CHEMOKINE LIKE FACTOR(CXCLF) WITH CHEMOTACTIC AND HEMATOPOIET  
; FILE REFERENCE: 10776-003-999  
; CURRENT APPLICATION NUMBER: US/09/801,115  
; PRIOR FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: PCT/CN00/00026  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 99107284.7  
; NUMBER OF SEQ ID NOS: 8  
; LENGTH: 459  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-801-115-3

Alignment Scores:  
Pred. No.: 2.13e-58 Length: 459  
Score: 471.50 Matches: 99  
Percent Similarity: 65.13% Conservative: 0  
Best Local Similarity: 65.13% Mismatches: 0  
Query Match: 92.81% Indels: 53  
DB: Gaps: 1

US-09-801-115b-2 (1-99) x US-09-801-115-3 (1-459)

Qy 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20  
Db 1 ATGGATTACGTGCAGCCGCAAAATATAACATGCGCCCTTCTGCTTCAAGTGAAGGCCAC 60  
Qy 21 ValLysMetLeuArg----- 25  
Db 61 GTGAAGAGTGTGGCGCTGATATATCACTGATGTAACAACAGATTCATCTCTATC 120  
Qy 25 ----- 25  
Db 121 GCCCGTAACCATATATTTGTTATCACTGGATTGAAGTACCGCTTATCTTTTCA 180  
Qy 26 -----Leuasp 27  
Db 181 CTTTATATGTAAGTCACTGATGATGATTAATGAAGTGTATTGCGCTTGTGAT 240  
Qy 28 IleIleAsnSerLeuValThrThrAlaPheMetLeuIleValSerValLeuAlaLeu 47  
Db 241 ATTATCACTGATGTAACAACAGATTCATGCTGATGTTGTGCTGCTGCTGCTGCTG 300  
Qy 48 ProGluThrThrThrLeuThValGlyGlyAlaPheAlaLeuValThrAlaValCys 67  
Db 301 CCAGAAACCAACAATTCAGTGTGTGGAGGGGTGTTGCACTGTGACACATATAC 360  
Qy 68 CysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSerGlyProTyr 87  
Db 361 TGTCTGTGGCGAGCGGGCCCTTATTACCGAAGCTTCTGTTCAATCCACGAGGCTTAC 420  
Qy 88 GlnLysLysProValHisGluLysLysGluValLeu 99  
Db 421 CAGAAAGACCTGTGTGATGAAAGAAAGATTG 456

RESULT 9  
US-09-978-295A-189  
; Sequence 189, Application US/09978295A  
; Patent No. US2002015606A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi



APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fond, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR FILING DATE: 1998-03-30  
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;; PRIOR FILING DATE: 1998-04-29  
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;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
Pred. No.: 3.66e-58 Length: 663  
Score: 471.50 Matches: 99  
Percent Similarity: 65.13% Conservative: 0  
Best Local Similarity: 65.13% Mismatches: 0  
Query Match: 92.81% Indels: 53  
DB: 9 Gaps: 1

US-09-801-115b-2 (1-99) x US-09-978-295A-189 (1-663)

Qy 1 MetaspasmyalginPolysiletyshlsarProphocysheserallysghlyhis 20  
Db 131 ATGATATACGTGACGCCGAAATTAACATCGCCCTTCCTTCAGTGGAAGCCAC 190  
Qy 21 VallysNelLeuarg----- 25  
Db 191 GTGAAGATGCTGGCGGCGACCTAAGTGACATCTATGACCTTTTATCATCGACAA 250  
Qy 25 ----- 25  
Db 251 GCCCTGACCATATATTTGTTATCACTGATTTGAAGTACCGTATCTTATTTTCANA 310

Qy 26 -----Leuasp 27  
Db 311 CTTTATATGATGACAGCTTGATCGATTAATGAGTGTATTATTTGGCCTTGCTTGAT 370  
Qy 28 IlelleasnerleuValThrThrValPheMetleuIleValserValleuAlaleuIle 47  
Db 371 ATTATCACTACACGCGGTGACACAGTATTATGCTCTCATCTGCTGTGGCAGTGATA 430  
Qy 48 ProgluThrThrThrleuThrValGlyGlyValPheAlaleuValThrAlaValcys 67  
Db 431 CCAGAAACCAACATGATGACAGTGTGGAGGGGTGTTCCACTTGAGACAGATATGC 490  
Qy 68 CysteualaspGlyAlaleuIleYrArglyleuIleuPheasnProserGlyProYr 87  
Db 491 TGCTTCCGACGGGGCCTTATTATACCGGAACTTGTCTCATTCACGCGGTCTTAC 550  
Qy 88 GluylsLysProValHisGluylsGluValleu 99  
Db 551 CAGAAAGCCTGTCATGAAAGAAAGTTTG 586

RESULT 10  
US-09-978-697-189  
; Sequence 189, Application US/09978697  
; Patent No. US20020169284A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Bolstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Geo, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoul, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2650PIC27  
; CURRENT APPLICATION NUMBER: US/09/978,697  
; PRIOR FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649	PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791	PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004	PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886	PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936	PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910	PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939	PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294	PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656	PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664	PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689	PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663	PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079923	PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105	PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107	PRIOR FILING DATE: 1998-03-31
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PRIOR APPLICATION NUMBER: 60/080334	PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070	PRIOR FILING DATE: 1998-04-08
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PRIOR APPLICATION NUMBER: 60/081195	PRIOR FILING DATE: 1998-04-08
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PRIOR APPLICATION NUMBER: 60/081955	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817	PRIOR FILING DATE: 1998-04-15
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PRIOR APPLICATION NUMBER: 60/081952	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838	PRIOR FILING DATE: 1998-04-15
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PRIOR APPLICATION NUMBER: 60/082569	PRIOR FILING DATE: 1998-04-21

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3	PRIOR FILING DATE: 1998-04-22
4	PRIOR APPLICATION NUMBER: 60/082804
5	PRIOR FILING DATE: 1998-04-22
6	PRIOR APPLICATION NUMBER: 60/082700
7	PRIOR FILING DATE: 1998-04-22
8	PRIOR APPLICATION NUMBER: 60/082797
9	PRIOR FILING DATE: 1998-04-22
10	PRIOR APPLICATION NUMBER: 60/082796
11	PRIOR FILING DATE: 1998-04-23
12	PRIOR APPLICATION NUMBER: 60/083336
13	PRIOR FILING DATE: 1998-04-27
14	PRIOR APPLICATION NUMBER: 60/083322
15	PRIOR FILING DATE: 1998-04-28
16	PRIOR APPLICATION NUMBER: 60/083392
17	PRIOR FILING DATE: 1998-04-29
18	PRIOR APPLICATION NUMBER: 60/083495
19	PRIOR FILING DATE: 1998-04-29
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21	PRIOR FILING DATE: 1998-04-29
22	PRIOR APPLICATION NUMBER: 60/083499
23	PRIOR FILING DATE: 1998-04-29
24	PRIOR APPLICATION NUMBER: 60/083545
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69	PRIOR FILING DATE: 1998-05-15
70	PRIOR APPLICATION NUMBER: 60/085580
71	PRIOR FILING DATE: 1998-05-15
72	PRIOR APPLICATION NUMBER: 60/085573
73	PRIOR FILING DATE: 1998-05-15

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[illegible]

PRIOR FILING DATE: 1998-04-01  
 PRIOR APPLICATION NUMBER: 60/081070  
 PRIOR FILING DATE: 1998-04-08  
 PRIOR APPLICATION NUMBER: 60/081049  
 PRIOR FILING DATE: 1998-04-08  
 PRIOR APPLICATION NUMBER: 60/081071  
 PRIOR FILING DATE: 1998-04-08  
 PRIOR APPLICATION NUMBER: 60/081195  
 PRIOR FILING DATE: 1998-04-08  
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 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084639  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084640  
 PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/084598  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084627  
 PRIOR FILING DATE: 1998-05-07  
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 PRIOR APPLICATION NUMBER: 60/085689  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085579  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085580  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
 Pred. No.: 3,66e-58 Length: 663  
 Score: 471.50 Matches: 99  
 Percent Similarity: 65.13% Conservative: 0  
 Best Local Similarity: 65.13% Mismatches: 0  
 Query Match: 92.81% Indels: 53  
 DB: 9 Gaps: 1

US-09-801-115b-2 (1-99) x US-09-978-192A-189 (1-663)

QY 1 MetaspasnaValInpPolysIleIysHIsArpProheCyPheSerValIysGlyHIs 20  
 DB 131 ATGATACGTCGCGACCGGAAATATACATCGCCCTTCTGCTTCACTGTAAGGCGAC 190  
 QY 21 ValIysMeLeuArg----- 25  
 DB 191 GTGAAGATGCTGCGGCGGCGACACTAGCTGACATCTATGACCTTTTATCATCGACAA 250  
 QY 25 ----- 25  
 DB 251 GCCCCTGAAACATATATTTATTCACGTGATTGAACTGACCGTTATCTATTTTCATA 310  
 QY 26 -----LeuAsp 27  
 DB 311 CTTTATATATGACACACTGATCGATTAATGAAGTGTTATTTGGCCTTGTGAT 370  
 QY 28 IleIleasnSerIleuValThrValIpheMeLeuIleValSerValIleuAlaLeuIle 47  
 DB 371 ATTATCACTGACGTGATCAACAGATATTCATGCTCATCGATCTGTGGCAGTGATA 430  
 QY 48 ProGUThrThrThrIleuThrValGlyGlyValIleAlaLeuValThrAlaValCys 67  
 DB 431 CCAGAAACCAACATTTACAGTTGGTGGAGGGGTGTTGGACTGTGACAGCGATATGC 490  
 QY 68 CysLeuAlaAspGlyAlaLeuIleTyraGlySerLeuIleuPheAsnProSerGlyProTyr 87  
 DB 491 TGTCTTGGCGAGGGGCCCTTATTTACCGAAGCTTGTGTCATCCAGGGGCTTAC 550  
 QY 88 GlnIysIysProValIleIleGlyIysGlyValIleu 99  
 DB 551 CAGAAAGCCTGTCATGAGAAAAAGAAAGAGTTTGG 586

RESULT 12

US-09-999-832A-189  
Sequence 189, Application US/0999832A  
Publication No. US20020192706A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Iyar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC63  
CURRENT APPLICATION NUMBER: US/09/999,832A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
Pred. No.: 3,66e-58 Length: 663  
Score: 471.50 Matches: 99  
Percent Similarity: 65.13% Conservative: 0  
Best Local Similarity: 65.13% Mismatches: 53  
Query Match: 92.81% Indels: 53  
DB: 9 Gaps: 1

US-09-801-115b-2 (1-99) x US-09-999-832A-189 (1-663)

QY 1 MetaspasynValInProlysilLeuSHsArgProPheCysPheSerValIysGlyHis 20  
Db 131 ATGATTAACGTCGACGCGAATAAACAATCGCCCTTCGCTTGTGAAGGCCAC 190  
QY 21 ValIysMetLeuArg----- 25  
Db 191 GTGAAGATGCTGCGGCTGCACACTAAGTCATGATGACCTTTTATCATCGACAA 250

QY 25 ----- 25  
Db 251 GCCCCTGAACCATATATGTTATCATGACTGATTTGAAGTCAACCGTATATTTTCATA 310  
QY 26 -----LeuAsp 27  
Db 311 CTTTATATGTAATGACTACAGCTTGATGATTAATGAAGTGTATTTTGGCCTTGCTGAT 370  
QY 28 IleIleAsnSerLeuValIleThrValPheMetLeuIleValSerValIleValIle 47  
Db 371 ATTATCAACTACACGTAACACAGATTCATGCTCACTATCTGTGTGGACATGATA 430  
QY 48 ProGluThrThrThrIleThrValIleGlyIleValPheAlaLeuValIleAlaValCys 67  
Db 431 CCAGAAACCAACCAATGACAGTGTGTGAGAGGCTGTTCCACTGTGACAGCATATGC 490  
QY 68 CysLeuAlaAspGlyAlaLeuIleTyrArgIysLeuLeuPheAsnProSerGlyProTyr 87  
Db 491 TGTCTGCCGACGAGGGGCGCTTATTTACCGAAGCTTCTGTCAATCCACAGGCTTAC 550  
QY 88 GluIysIysProValIleGluIysGluValIleu 99  
Db 551 CAGAAAAAGCCTGTGCATGAAAAAAGAGTTTG 586

RESULT 13  
US-09-978-189-189  
Sequence 189, Application US/09978189  
Publication No. US20030004102A1

GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
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APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavaric, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paonli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C7  
CURRENT APPLICATION NUMBER: US/09/978,189  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
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PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450

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2	PRIOR FILING DATE: 1998-04-15
3	PRIOR APPLICATION NUMBER: 60/082566
4	PRIOR FILING DATE: 1998-04-21
5	PRIOR APPLICATION NUMBER: 60/082566
6	PRIOR FILING DATE: 1998-04-21
7	PRIOR APPLICATION NUMBER: 60/082704
8	PRIOR FILING DATE: 1998-04-22
9	PRIOR APPLICATION NUMBER: 60/082804
10	PRIOR FILING DATE: 1998-04-22
11	PRIOR APPLICATION NUMBER: 60/082700
12	PRIOR FILING DATE: 1998-04-22
13	PRIOR APPLICATION NUMBER: 60/082797
14	PRIOR FILING DATE: 1998-04-22
15	PRIOR APPLICATION NUMBER: 60/082796
16	PRIOR FILING DATE: 1998-04-23
17	PRIOR APPLICATION NUMBER: 60/083363
18	PRIOR FILING DATE: 1998-04-23
19	PRIOR APPLICATION NUMBER: 60/083322
20	PRIOR FILING DATE: 1998-04-28
21	PRIOR APPLICATION NUMBER: 60/083392
22	PRIOR FILING DATE: 1998-04-29
23	PRIOR APPLICATION NUMBER: 60/083495
24	PRIOR FILING DATE: 1998-04-29
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26	PRIOR FILING DATE: 1998-04-29
27	PRIOR APPLICATION NUMBER: 60/083499
28	PRIOR FILING DATE: 1998-04-29
29	PRIOR APPLICATION NUMBER: 60/083545
30	PRIOR FILING DATE: 1998-04-29
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32	PRIOR FILING DATE: 1998-04-29
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38	PRIOR FILING DATE: 1998-04-29
39	PRIOR APPLICATION NUMBER: 60/083742
40	PRIOR FILING DATE: 1998-04-30
41	PRIOR APPLICATION NUMBER: 60/084366
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43	PRIOR APPLICATION NUMBER: 60/084414
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52	PRIOR FILING DATE: 1998-05-07
53	PRIOR APPLICATION NUMBER: 60/084598
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55	PRIOR APPLICATION NUMBER: 60/084600
56	PRIOR FILING DATE: 1998-05-07
57	PRIOR APPLICATION NUMBER: 60/084627
58	PRIOR FILING DATE: 1998-05-07
59	PRIOR APPLICATION NUMBER: 60/084643
60	PRIOR FILING DATE: 1998-05-07
61	PRIOR APPLICATION NUMBER: 60/085582
62	PRIOR FILING DATE: 1998-05-15
63	PRIOR APPLICATION NUMBER: 60/085700
64	PRIOR FILING DATE: 1998-05-15
65	PRIOR APPLICATION NUMBER: 60/085689
66	PRIOR FILING DATE: 1998-05-15
67	PRIOR APPLICATION NUMBER: 60/085579
68	PRIOR FILING DATE: 1998-05-15



; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085580  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085573  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085704  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.:	3,66e-58	Length:	663
Score:	471.50	Matches:	99
Percent Similarity:	65.13%	Conservative:	0
Best Local Similarity:	65.13%	Mismatches:	0
Query Match:	92.81%	Indels:	53
		Gaps:	1

US-09-801-115b-2 (1-99) x US-09-978-189-189 (1-663)

QY 1 MetaspasnaValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20  
 DB 131 ATGATTAAGCTGACACCCGAAATATAACATCGCCCTTCTGTTCACTGTAAGGCCAC 190  
 QY 21 ValLysMetLeuArg----- 25  
 DB 191 GTGAAGATGCTGCGCTGGCAGCTAGTGCATCTAGACCTTTTATCATCGCACAA 250  
 QY 25 ----- 25  
 DB 251 GCCCTGAACCATATATTGTATCATCTGATTTGAAGTACCGCTTATCTTATTTTCATA 310  
 QY 26 -----Leuasp 27  
 DB 311 CTTTATATATGACTCAGACTGATGATTAATGAAGTGTATTTTGCCCTTGTGAT 370  
 QY 28 IleIleasnSerLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle 47  
 DB 371 ATTATCAACTCAGTGTGTAACAACAGTATTCATGCTATCTGTGTGGCAGTATA 430  
 QY 48 ProGluThrThrThrLeuThrValGlyGlyValAlaPheAlaLeuValThrAlaValCys 67  
 DB 431 CCAGAAACCCACAACTTGACACTGTGTGGAGGGGCTTTGCACTTGACACAGTATGAC 490  
 QY 68 CysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheasnProSerGlyProTyr 87  
 DB 491 TGTCTTGGCGAGGGGCCCTTATTTACCGGAAGCTTGTCTCAATCCACAGGGGTCTTAC 550  
 QY 88 GlnLysLysProValHisGluLysGluValLeu 99  
 DB 551 CAGAAAAAGCCTGTGCATGAAAAAAGAAAGTTTGG 586  
 RESULT 14  
 ; US-09-978-608A-189  
 ; Sequence 189, Application US/09978608A  
 ; Publication No. US20030045462A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerlitsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2630PIC22  
 ; CURRENT APPLICATION NUMBER: US/09/978,608A  
 ; CURRENT FILING DATE: 2001-10-16  
 ; NUMBER OF SEQ ID NOS: 624  
 ; Prior Application removed - See File Wrapper or Palm  
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 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-978-608A-189

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US-09-801-115b-2 (1-99) x US-09-978-608A-189 (1-663)

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 ; Publication No. US20030050239A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
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APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerbert, Hanspeter  
APPLICANT: Geriltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Gunney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C4  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

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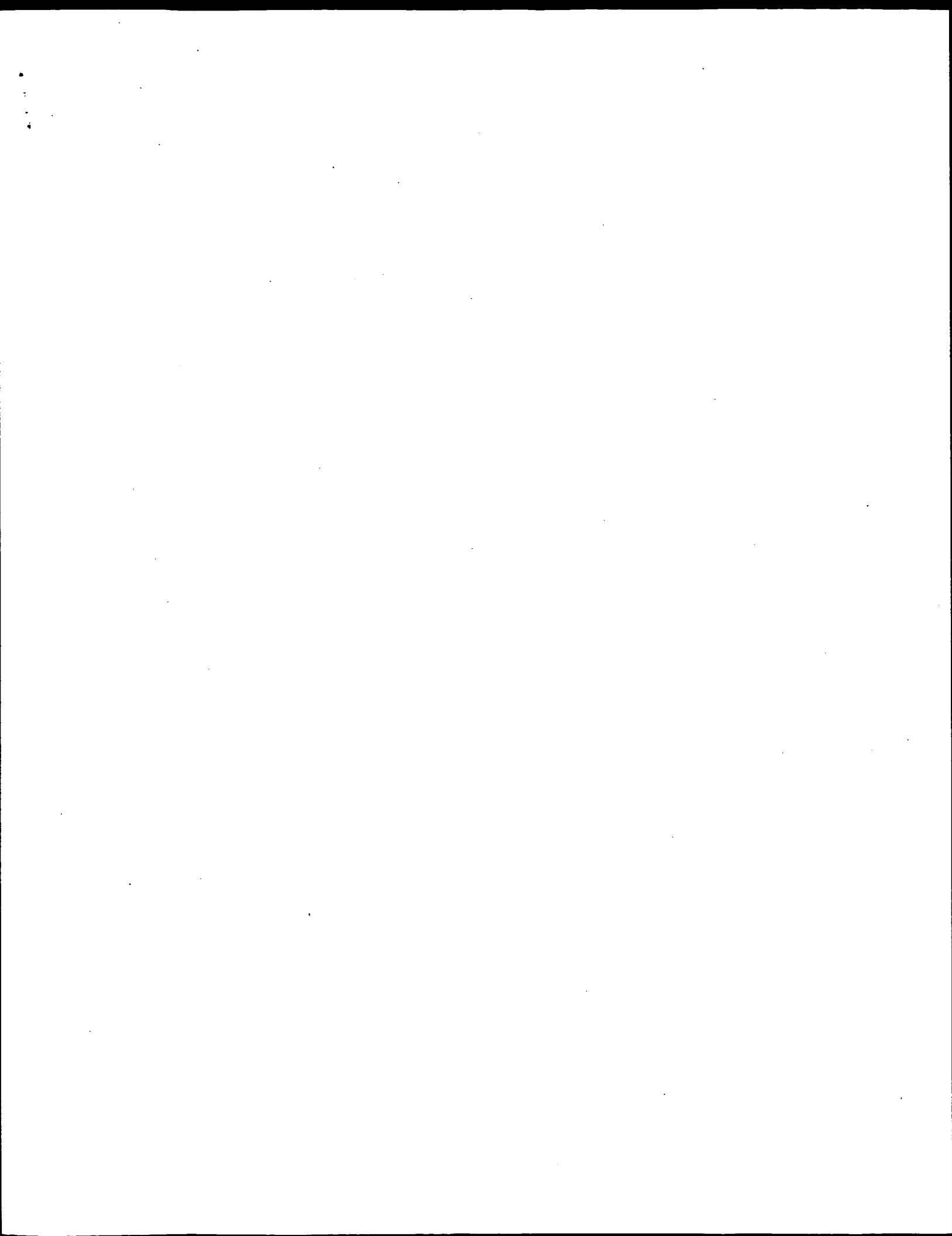
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Best Local Similarity: 65.13% Mismatches: 0  
Query Match: 92.81% Indels: 53  
DB: 9 Gaps: 1

US-09-801-115b-2 (1-99) x US-09-978-191a-189 (1-663)

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Db 131 ATGGATACGTCGACGCCGAAATAAACATCGCCCTTCGCTCACTGGAAGGCCAC 190  
Qy 21 ValLysMetLeuArg----- 25  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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ACCESSION AF096895  
VERSION AF096895.2 GI:9989691  
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ORGANISM Homo sapiens.  
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REFERENCE  
1 (bases 1 to 530)  
Han, W., Lou, Y., Tang, J., Zhang, Y., Li, Y., Gu, W., Huang, J.,  
Gul, L., Tang, Y., Li, F., Song, Q., Di, C., Wang, L., Shi, Q., Sun, R.,  
Xia, D., Rul, M., Tang, J., and Ma, D.

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TITLE      Molecular cloning and characterization of chemokine-like factor 1
            (CKLF1), a novel human cytokine with unique structure and potential
            chemotactic activity
JOURNAL    Biochem. J. 357 (Pt 1), 127-135 (2001)
MEDLINE    11415443
PUBMED     2 (bases 1 to 530)
REFERENCE  Han, W.L., Li, Y., Zhang, Y.M., Di, C.H., Song, Q.S. and Ma, D.L.
AUTHORS    Direct Submission
TITLE      Submitted (03-06-1998) Immunology, Beijing Medical University, 38
JOURNAL    Xue Yuan Rd., Beijing 100083, China
REFERENCE  3 (bases 1 to 530)
AUTHORS    Han, W.L.
TITLE      Direct Submission
JOURNAL    Submitted (07-SEP-2000) Immunology, Peking University Health
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            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 515)
            dumas mine Edwards, J.B., Bouguenel, L. and Jobert, S.
            Complementary dna's encoding proteins with signal peptides
            Patent: WO 0100806-A 29 04-JAN-2001;
            GENSEP (FR)
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BASE COUNT 143 a 106 c 135 g 130 t 1 others
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Best Local Similarity 99.4%; Pred. No. 1.1e-110;
Matches 505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY      15 GTGAAGCCGAGCTGGCGGAGAGTAGGGAGGGCGGTCTCCGCCGGTGGCGTTCCT 74
DB      8 GGGAAAGCCGAGCTGGCGGAGAGTAGGGAGGGCGGTCTCCGCCGGTGGCGTTCCT 66
QY      75 ATGCGTTGCGAAGCTACCTACGACGACGACGACGACGACGACGACGACGACGACGAC 134
DB      67 ATGCGTTGCGAAGCTACCTACGACGACGACGACGACGACGACGACGACGACGACGAC 126
QY      135 CTGGGTCTGACAGCGGATGATACGTGACGACGACGACGACGACGACGACGACGACGAC 194
DB      127 CTGGGTCTGACAGCGGATGATACGTGACGACGACGACGACGACGACGACGACGACGAC 186
QY      195 TCAAGTGTGAAGGCGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 254
DB      187 TCAAGTGTGAAGGCGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 246
QY      255 CAGATATTCATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 314
DB      247 CAGATATTCATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 306
QY      315 TTGGTGGAGGGGTGTTGCACTGTGACAGCAGATATGCTGCTTGGCGAGGGGCCCTTA 374
DB      307 TTGGTGGAGGGGTGTTGCACTGTGACAGCAGATATGCTGCTTGGCGAGGGGCCCTTA 366
QY      375 TTATACCGGAAGCTTCTTCAATCCAGCGGCTCTTACAGAAAAGCCTGTGCATGAAA 434
DB      367 TTATACCGGAAGCTTCTTCAATCCAGCGGCTCTTACAGAAAAGCCTGTGCATGAAA 426

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QY	495	TCTGTATTCTTCCAAAAAATTTTAAAAA	522
Db	487	TCTGTATTCTTCCAAAAAATTTTAAAAA	514
RESULT 3			
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AF135380			PRI 07-SEP-2000
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REMARK			
COMMENT			
FEATURES			
SOURCE			
gene			
CDS			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
QY	15	GTGAAGCCGAGCTGGGCGACAGAAAGTAGGAGGAGGCGGCTCTCCGCCGCGTGGCGGTCT	74
Db	11	GGGAAGCCGAGCTGGGCGACAGAAAGTAGGAGGAGGCGGCTCTCCGCCGCGTGGCGGTCT	70
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Db	71	ATCGCTTGACAGAACTACTACGAGCAGCAGCTGAGAGAGTGAAGGAAAGTGCCTG	130
QY	135	CTGGGTCTGCACAGCGATGATTAACGTGCACCGCAAAATATAAATCATGCCCCCTTCTGCT	194
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Db	191	TCAGTGTGAAGGCCACGTAAGTGGTGGCGGACACTAAGTGTGACATCTATGACCT	250		
QY	230	-----	229		
Db	251	TTTTTATCATGCAACAAGCCCTGAACCATATATTTGTTACTGATTTGAAGTACCG	310		
QY	230	-----	229		
Db	311	TTATCTTATTTTTCATACTTTTATNGTACTGACACTTGATTCGATTATGCAAGTGGTTAT	370		
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QY	276	CTGTGTGGGCACTGATACCAAGAAACCAACAATTGACAGTTGGTGGAGGGGTGTTGGAC	335		
Db	431	CTGTGTGGGCACTGATACCAAGAAACCAACAATTGACAGTTGGTGGAGGGGTGTTGGAC	490		
QY	336	TTTGGACAGCAGTGTGCTGCTGTCCGACGAGGGGCCCTTATTTACCGGAGCTTGTTCA	395		
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QY	396	ATCCACAGGCGCTTACACAGAAAGCCCTGTGATGAAAAAAGAAAGTTTGTATTTT	455		
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QY	456	ATATTACTTTTAACTTTGATGATGATTAAGATTTTCTGTATTTCTCCAAAAAAA	515		
Db	611	ATATTACTTTTAACTTTGATGATGATTAAGATTTTCTGTATTTCTCCAAAAAAA	670		
QY	516	AAAAAAAAAAAAAAAAAAAAA	534		
Db	671	AAAAAAAAAAAAAAAAAAAAA	689		
RESULT 4	AF145216	593 bp	mrna	linear	PRI 07-SEP-2000
LOCUS	AF145216				
DEFINITION	Homo sapiens chemokine-like factor 4 (CKLF4) mRNA, complete cds,				
ACCESSION	AF145216				
VERSION	AF145216.2	GI:9989694			
KEYWORDS					
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 593)				
AUTHORS	Han,W.L., Gu,W.F., Li,Y., Zhang,Y.M., Di,C.H., Song,Q.S. and Ma,D.L.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-APR-1999) Immunology, Beijing Medical University, Xue				
REFERENCE	Yuan Road, Beijing 100083, China				
AUTHORS	2 (bases 1 to 593)				
TITLE	Han,W.L.				
JOURNAL	Direct Submission				
REFERENCE	Submitted (07-SEP-2000) Immunology, Peking University Health				
AUTHORS	Science Center, Xueyuan Road 38, Beijing 100083, China				
JOURNAL	Sequence update by submitter				
REMARK	On Sep 7, 2000 this sequence version replaced gi:6625671.				
COMMENT	location/Qualifiers				
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BASE COUNT      166 a      120 c      140 g      167 t
ORIGIN
Query Match      65.4%; Score 349; DB 9; Length 593;
Best Local Similarity 79.8%; Pred. No. 3.4e-75;
Matches 465; Conservative 0; Mismatches 55; Indels 63; Gaps 2;
15 GTGAAGCCGAGCTGGGCGAGAGTAGAGGAGGCGGTCTCCGCGGCTGGCTCT 74
11 GGGAGCCGAGCTGGGCGAGAGTAGAGGAGGCGGTCTCCGCGGCTGGCTCT 70
75 ATCCGCTCGCAACACCTACTCAGCGACGCTGAGAAAGTTGAGGAGAGTCTGCTG 134
71 ATCCGCTCGCAACACCTACTCAGCGACGCTGAGAAAGTTGAGGAGAGTCTGCTG 130
135 CTGGGCTCGCAACGCGATGATACGTCGAGCGGAGAAATAAACATGCCCTTCTGCT 194
131 CTGGGCTCGCAACGCGATGATACGTCGAGCGGAGAAATAAACATGCCCTTCTGCT 190
195 TCAGTGTGAAAGGCGACGTAAGATGCTCGCGCTGG----- 230
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231 -----ATATATCACTCACTGCTGTAACACAG 257
251 TTTTATCATCGCACAGACCCCTGACCATATATGTTATCATCGATTTGAGTACACCG 310
258 TATTCATGCTCATCTATCTGTTGTCGACATGATACAG-----AACACACATTTGA 311
311 TTAATCTTATTTTCACTTTTATATGATGACACTGATGATTAATGAAGTGTAT 370
312 CAGTGTGAGAGGGGTGTTGCACTTGTGACAGCAGATAGCTGCTTCCGACGCGGCC 371
371 TTTGGCTTTGCTGTTGTTGCTGACAGCAGATAGCTGCTTCCGACGCGGCC 430
372 TTAATTCGCGAGAGTGTGTTCAATCCAGCGGCTTACCACAAAAAGCTTGATG 431
431 TTAATTCGCGAGAGTGTGTTCAATCCAGCGGCTTACCACAAAAAGCTTGATG 490
432 AAAAAAAGAGTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 491
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RESULT 5  
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 DEFINITION Homo sapiens, clone MGC:10658 IMAGE:3639550, mRNA, complete cds.  
 ACCESSION BC004380  
 VERSION BC004380.1 GI:13325133  
 KEYWORDS MGC.  
 SOURCE  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE Submitted (12-MAR-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

REMARK  
 COMMENT  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 BC Sequencing by: Genome Sequence Centre,  
 BC Cancer Agency, Vancouver, BC, Canada  
 info@bcsc.bc.ca  
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
 Letlicia Hsiao, Martin Krzywinski, Retz Kische, Oliver Lee, Soo  
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven  
 Ness, Pawan Pandoh, Anna-Liisa Prabh, Parvaneh Saeedi, Jacqueline  
 Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott,  
 Michael Thorne, Miranada Tsal, Natsija van den Bosch, Jill Vardy,  
 George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
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BASE COUNT 201 a 138 c 154 g 195 t  
 ORIGIN

Query Match 63.3%; Score 338; DB 9; Length 688;  
 Best Local Similarity 76.1%; Pred. No. 1.7e-72;  
 Matches 507; Conservative 0; Mismatches 0; Indels 155; Gaps 1;

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28 GGGCGAAGATGAGGAGGCGGTCTCCGCGGCTGGCTGCTATGCTGCGAGA 87
13 GGGCGAAGATGAGGAGGCGGTCTCCGCGGCTGGCTGCTATGCTGCGAGA 72
88 ACTTACTCAGGCGAGCTGAGAGAGTTGAGGAGAAAGTGTGCTGGCTGCGAGA 147
73 ACTTACTCAGGCGAGCTGAGAGAGTTGAGGAGAAAGTGTGCTGGCTGCGAGA 132
148 CGGATGATTAACGTCACCGCAAAATAAACATCGCCCTTCTCTCACTGAGAAAG 207
133 CGGATGATTAACGTCACCGCAAAATAAACATCGCCCTTCTCTCACTGAGAAAG 192
208 CCACTGATGATGCTGGCGCTG----- 229
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230 ----- 229
253 ACAAGCCCTGACCAATATATGTTATACAGTGAAGTTGAAGTGAAGTTGAAGTTGA 312
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Db	433	GATACCCAGAAACCACACACATTGAGACAGTTGGTGGAGGGGTGTTGCATCTGTGACACAGT	492
QY	349	ATGCTGCTTCCACACGGGGCCCTTATTTTACCGGAGCTTGTCATCCACACGGGTC	408
Db	493	ATGCTGCTTCCACACGGGGCCCTTATTTTACCGGAGCTTGTCATCCACACGGGTC	552
QY	409	TTACACAGAAAAAGCCTGTGTCATGAAAAAAGAAGTTTGTAATTTATATACCTTTTA	468
Db	553	TTACACAGAAAAAGCCTGTGTCATGAAAAAAGAAGTTTGTAATTTATATACCTTTTA	612
QY	469	GTTTGATGCTAAGTATTAAACATATTTCTGATTTCTCCAAAAAATTTTTTTTTT	528
Db	613	GTTTGATGCTAAGTATTAAACATATTTCTGATTTCTCCAAAAAATTTTTTTTTT	672
QY	529	AAAAA 534	
Db	673	AAAAA 678	
RESULT 6			
LOCUS	AF057306	655 bp	mrna linear PRI 31-DEC-1999
DEFINITION	Homo sapiens transmembrane proteolipid (C32) mrna, complete cds.		
ACCESSION	AF057306		
VERSION	AF057306.1	GI:6648618	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 655)		
TITLE	Zhang, J.S., Nelson, M., Wang, L. and Smith D.I.		
JOURNAL	Direct Submission		
FEATURES	Submitted (03-ARR-1998) Pathology and Lab. Medicine, Mayo Clinic and Foundation, Rochester, MN 55905, USA		
SOURCE	Location/Qualifiers		
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CDS	132..590		
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BASE COUNT	171 a 137 c 153 g 194 t		
ORIGIN			
Query Match	60.9%; Score 325.4; DB 9; Length 655;		
Best Local Similarity	75.6%; Pred. No. 2,1e-69;		
Matches	495; Conservative 0; Mismatches 1; Indels 159; Gaps 1;		
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QY	81	TCGAGAAACCTACTCAGGCACGACGCTGAGAAAGTTGAGGAAAGTCTGCTGGGCT	140
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QY		141	CTGCAGACGGCATGTGATTAACGTGCAGGCCGAATAAATCAATCGCCCTTCGCTTCACTG	200
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Dd		181	TGAAAGGCCACGTGAAGATGCTGGCGCTGGCAGCTAACGTGACATCTATGACCTTTTSTA	240
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QY		230	-----GATATTATCACTCACTGGTGTACACAGATTTTCATGCTCATCTGTGT-	281
Dd		361	CTTTGCTWTGATATATCACTCACTGGTGTACACAGATTTTCATGCTCATCTGTGTGT	420
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QY		342	CAGCAGATATGCTGCTTGGCGACGGGGCCCTTATTTACCGGAACCTTCGTTCAATCCA	401
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QY		462	CTTTTGTGTTGATCTAGATTAACAATTTCTGTATCTTCCAAAAAANA	516
Dd		601	CTTTTGTGTTGATCTAGATTAACAATTTCTGTATCTTCTAAAAAANA	655

RESULT 7

AX061665

LOCUS

DEFINITION Sequence 70 from Patent WO0100806.

ACCESSION AX061665

VERSION AX061665.1 GI:12406789

KEYWORDS

SOURCE

ORGANISM

human.

human sapiens

Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS dumas mine Edwards,J.B., Bougueleret,L., and Jobert,S.

TITLE Complementary dna's encoding proteins with signal peptides

JOURNAL Patient: WO 0100806-A 70 04-JAN-2001;

GENSET (FR)

FEATURES

source

Location/Qualifiers

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/db\_xref="taxon:9606"

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/note="Von Heijne matrix score 4..10 seq VFMLISVALIIP/ET"

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polya\_site

655..669

BASE COUNT

ORIGIN

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158 g

194 t



SOURCE Homo sapiens.  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 485)  
JOURNAL Myers, R.M.  
COMMENT Unpublished (1996)

Contact: Richard M. Myers  
Stanford Human Genome Center (SHGC)  
Stanford University School of Medicine  
Department of Genetics, M-344, Stanford, CA 94305, USA  
Tel: 4157259687  
Fax: 4157259689  
Email: myerseshgc.stanford.edu

Primer A: ACTCTCTTTTTCATGCACAGG  
Primer B: GCCCTTATTACCGAAGCT  
STS size: 77  
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds  
Denaturation: 94 degrees C for 15 seconds  
Annealing: 62 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9600

Protocol:  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Tag Polymerase: 0.05 units/uL  
Total Vol: 10 uL

Buffer:  
MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from T90565  
-- Washington University/Merck EST sequence.

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Matches 281; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 227 ACTGATACAGAAACCAACATTTGACAGTTGTGAGAGGGGTTCCTACTTGACAGC 168  
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DB 167 AGTATGCTGTTGCCAGCGGGCCCTTATTATTCGGAAGCTTGTGTAATCCACGG 108  
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DB 107 TCCATACAGAAAGCGCTGTGATGAAAGAAAGTTTGAATTTATTTATTTACTTT 48

QY 466 TTAGTTGATACACTATTAACATATTTCTGATCTTCCAAAA 512  
DB 47 TTAGTTGATACACTATTAACATATTTCTGATCTTATATATAA 1

RESULT 10  
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LOCUS Homo sapiens chromosome 16 clone CTA-989P12, complete sequence.  
DEFINITION  
AC010289  
AC010289.9 GI:15451657  
KEYWORDS  
HTG.  
SOURCE  
Homo sapiens.  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 97083)  
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.  
JOURNAL Unpublished  
2 (bases 1 to 97083)  
AUTHORS DOE Joint Genome Institute.  
TITLE Direct Submission  
JOURNAL Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
3 (bases 1 to 97083)  
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE Direct Submission  
JOURNAL Submitted (24-OCT-2000) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
4 (bases 1 to 97083)  
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE Direct Submission  
JOURNAL Submitted (09-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
5 (bases 1 to 97083)  
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE Direct Submission  
JOURNAL Submitted (10-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
6 (bases 1 to 97083)  
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE Direct Submission  
JOURNAL Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
On Sep 6, 2001 this sequence version replaced gi:15147148.  
Draft Sequence Produced by DOE Joint Genome Institute  
www.jgi.doe.gov  
Finishing Completed at Stanford Human Genome Center  
www-shgc.stanford.edu  
Quality: Phrap Quality >=40 99.8% of Sequence;  
Estimated Total Number of Errors is 0.2.  
STS Content:  
WI-11439 G23701  
WI-15863 G24307  
WI-11780 G23805  
NOTE: A bacterial transposon was excised from this clone at  
position 96045.

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Best Local Similarity 99.5%; Pred. No. 8.5e-42;  
Matches 215; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 GTAAAGCCAGCTGGCGGAGAGTAGGAGGGGCTGCTCCGCCGCGGTGCTGCT 74  
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Db 6753 GGGAGCCGAGCTGGGCGAGAGTAGAGGAGGCGGTCTCCGCGCGGTGGCTGCT 6694

QY 75 ATCGCTTCGAGAACCTACTACAGGCGCCAGCTGAGAGAGTTGAGGGAGAGTGGCTG 134

Db 6693 ATCGCTTCGAGAACCTACTACAGGCGCCAGCTGAGAGAGTTGAGGGAGAGTGGCTG 6634

QY 135 CTGGGCTCTCAGACGGGATGATTAACGTGACAGCCGAAATAAAGATGCGCCCTTCTGCT 194

Db 6633 CTGGGCTCTCAGACGGGATGATTAACGTGACAGCCGAAATAAAGATGCGCCCTTCTGCT 6574

QY 195 TCAGTGTGAAGGCCACGCTGAAGATGCTCGGCTG 230

Db 6573 TCAGTGTGAAGGCCACGCTGAAGATGCTCGGCTG 6538

RESULT 11

AC018589/c

LOCUS AC018589 151620 bp DNA linear HTG 30-MAR-2000

DEFINITION Homo sapiens clone RP11-13P4, WORKING DRAFT SEQUENCE, 18 unordered pieces.

ACCESSION AC018589

VERSION AC018589.3 GI:7341919

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 151620)

AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Homo sapiens, clone RP11-13P4

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 151620)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abram,H., Allen,N., Bogenbuhl,J., Boudgaltier,B., Brown,A., Burkett,G., Castle,A., Choeppel,X., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeRubeis,K., Dewar,K., Domingo,M., Doyle,M., Fenesbor,J., Garayna,S., Grant,G., Hagos,B., Heatford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Landers,T., Lebecky,J., Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Margulis,N., McEwan,P., McClure,A., McKernan,K., Meltrin,J., Menes,L., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Olivari,T.M., Peterson,K., Pierre,N., Pisanl,C., Pollara,V., Raymond,C., Riley,R., Rothman,D., Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

COMMENT Direct Submission

Submitted (14-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 30, 2000 this sequence version replaced gi:6692322.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Web site: http://www-seq.wi.mit.edu

Center code: MIBR

Contact: sequence\_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L3379

Center clone name: L3\_P4

----- Summary Statistics

Sequencing vector: M13: M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 141737 bases at least Q40

Consensus quality: 145736 bases at least Q30

Consensus quality: 147339 bases at least Q20

Insert size: 182000; agarose-fp

Insert size: 149920; sum-of-contigs

Quality coverage: 4.6 in Q20 bases; agarose-fp

Quality coverage: 5.5 in Q20 bases; sum-of-contigs

-----

\* NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1331: contig of 1331 bp in length

1332 1431: gap of 100 bp

1432 2326: contig of 895 bp in length

2327 2426: gap of 100 bp

2427 4519: contig of 2093 bp in length

4520 4619: gap of 100 bp

4620 6916: contig of 2297 bp in length

6917 7016: gap of 100 bp

7017 10850: contig of 3834 bp in length

10851 10950: gap of 100 bp

10951 15157: contig of 4207 bp in length

15158 15257: gap of 100 bp

15258 17752: contig of 2495 bp in length

17753 17852: gap of 100 bp

17853 22482: contig of 4630 bp in length

22483 22583: gap of 100 bp

22583 25540: contig of 3958 bp in length

25541 26640: gap of 100 bp

26641 30917: contig of 4277 bp in length

30918 31017: gap of 100 bp

31018 36401: contig of 5384 bp in length

36402 36501: gap of 100 bp

36502 42254: contig of 5753 bp in length

42255 42354: gap of 100 bp

42355 52974: contig of 10620 bp in length

52975 53074: gap of 100 bp

53075 62475: contig of 9401 bp in length

62476 62575: gap of 100 bp

62576 72661: contig of 10086 bp in length

72662 72761: gap of 100 bp

72762 89410: contig of 16649 bp in length

89411 89510: gap of 100 bp

89511 113391: contig of 23881 bp in length

113392 113491: gap of 100 bp

113492 151620: contig of 38129 bp in length.

Location/Qualifiers

1. 151620

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="RP11-13P4"

/clone.lib="RPC1-11 Human Male BAC"

1. 1331

/note="assembly\_fragment"

1432. 2326

/note="assembly\_fragment"

clone\_end:77

vector\_side:right"

2427. 4519

/note="assembly\_fragment"

4620. 6916

/note="assembly\_fragment"

7017. 10850

/note="assembly\_fragment"

10951. 15157

/note="assembly\_fragment"

15258. 17752

/note="assembly\_fragment"

17853. 22482

/note="assembly\_fragment"

22583. 26540

/note="assembly\_fragment"

26641. 30917



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QY      423 CTGTGCATGAAAAAAGAGTTTGTAAATTTATATTTACTTTAGTTGATCTAAGT 482
Db      87 CTGTGCATGAAAAAAGAGTTTGTAAATTTATATTTACTTTAGTTGATCTAAGT 28
QY      483 ATTAACATATTTCTGTATCTTCCA 508
Db      27 ATTAACATATTTCTGTATCTTCCA 2

RESULT 14
AX330787/c      207 bp      DNA      linear      PAT 09-JAN-2002
LOCUS      AX330787
DEFINITION      Sequence 1296 from Patent WO0194629.
ACCESSION      AX330787
VERSION      AX330787.1 GI:18103765
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1
AUTHORS      Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE      Cancer gene determination and therapeutic screening using signature
JOURNAL      Patent: WO 0194629-A 1296 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source      location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT      70 a      43 c      39 g      54 t      1 others
ORIGIN

Query Match      38.4%; Score 205; DB 6; Length 207;
Best Local Similarity 99.5%; Pred. No. 6.5e-40;
Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      303 CAACATTGACAGTTGGTGGAGGGGTTGCACTTGACAGCAGATGCTGTGCGG 362
Db      207 CAACATTGACAGTTGGTGGAGGGGTTGCACTTGACAGCAGATGCTGTGCGG 148
QY      363 ACGGGGCCCTTATTTACCGAAGCTCTGTCATCCCGAGCGGCTTACCGAGNAAAAGC 422
Db      147 ACGGGGCCCTTATTTACCGAAGCTCTGTCATCCCGAGCGGCTTACCGAGNAAAAGC 88
QY      423 CTGTGCATGAAAAAAGAGTTTGTAAATTTATATTTACTTTAGTTGATCTAAGT 482
Db      87 CTGTGCATGAAAAAAGAGTTTGTAAATTTATATTTACTTTAGTTGATCTAAGT 28
QY      483 ATTAACATATTTCTGTATCTTCCA 508
Db      27 ATTAACATATTTCTGTATCTTCCA 2

RESULT 15
AX331008      207 bp      DNA      linear      PAT 09-JAN-2002
LOCUS      AX331008/c
DEFINITION      Sequence 1517 from Patent WO0194629.
ACCESSION      AX331008
VERSION      AX331008.1 GI:18121642
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1
AUTHORS      Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE      Cancer gene determination and therapeutic screening using signature

```

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JOURNAL      Patent: WO 0194629-A 1517 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source      location/Qualifiers
1..207
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT      70 a      43 c      39 g      54 t      1 others
ORIGIN

Query Match      38.4%; Score 205; DB 6; Length 207;
Best Local Similarity 99.5%; Pred. No. 6.5e-40;
Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      303 CAACATTGACAGTTGGTGGAGGGGTTGCACTTGACAGCAGATGCTGTGCGG 362
Db      207 CAACATTGACAGTTGGTGGAGGGGTTGCACTTGACAGCAGATGCTGTGCGG 148
QY      363 ACGGGGCCCTTATTTACCGAAGCTCTGTCATCCCGAGCGGCTTACCGAGNAAAAGC 422
Db      147 ACGGGGCCCTTATTTACCGAAGCTCTGTCATCCCGAGCGGCTTACCGAGNAAAAGC 88
QY      423 CTGTGCATGAAAAAAGAGTTTGTAAATTTATATTTACTTTAGTTGATCTAAGT 482
Db      87 CTGTGCATGAAAAAAGAGTTTGTAAATTTATATTTACTTTAGTTGATCTAAGT 28
QY      483 ATTAACATATTTCTGTATCTTCCA 508
Db      27 ATTAACATATTTCTGTATCTTCCA 2

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Search completed: June 25, 2003, 11:30:38  
 Job time : 1529 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 05:32:44 ; Search time 217 Seconds

(without alignments)  
5541.784 Million cell updates/sec

Title: US-09-801-115B-1

Perfect score: 534  
Sequence: 1 gtcccaatctgagtggaag.....aaaaaaaaaaaaaaaaaaaaa 534

Scoring table: IDENTITY\_NNC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_101002:\*

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:\*
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- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:\*
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- 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	534	100.0	534	AAA38006	UCK-1 nucleotide s
2	507	94.9	655	AA344932	CDNA encoding nove
3	498.2	93.3	538	AAH98515	Human EST-derived
4	498.2	93.3	538	AAH98548	Human EST-derived
5	497.2	93.1	558	AAH34835	Human colon cancer
6	493.4	92.4	515	AAH87730	Human secreted pro
7	493.4	92.4	515	AAH64012	CDNA encoding huma
8	486.6	91.1	504	AAV59598	Human secreted pro
9	478.6	89.6	506	AAV59746	Human secreted pro

10	466.8	87.4	500	20	AAK97826	Human secreted pro
11	465.4	87.2	467	21	AAAI5929	Human protein clon
12	425	79.6	439	24	ABK36006	CDNA sequence #397
13	411.4	77.0	413	20	AAK97873	Human secreted pro
14	405.4	75.9	415	21	AAK00147	Human secreted pro
15	335	62.7	663	21	AAK34051	Human PRO772 nucle
16	335	62.7	663	21	AAK78498	Human PRO772 nucle
17	335	62.7	663	21	AAK58238	CDNA encoding nove
18	327.2	61.3	908	22	AAK44933	Human secreted pro
19	321.8	60.3	669	22	AAK87771	CDNA encoding huma
20	321.8	60.3	669	22	AAK64053	Human secreted pro
21	309.8	58.0	354	20	AAK41509	Human transmembran
22	309	57.9	637	21	AAK56747	Human polynucleoti
23	306.6	57.4	670	24	ABL90366	CDNA sequence #275
24	305.8	57.3	638	24	ABK35884	CDNA encoding nove
25	300	56.2	566	22	AAK45120	CDNA encoding nove
26	300	56.2	566	22	AAK45121	CDNA encoding nove
27	295.4	55.3	297	21	AAAI5919	Human prostate clon
28	285	53.4	544	23	ABV56930	Human prostate exp
29	272	50.9	392	21	AAAI6090	Human colon cancer
30	224.4	42.0	459	21	AAK38007	UCK-2 nucleotide s
31	214.4	40.1	5021	22	AAK82407	Human immune/haema
32	214.4	40.1	13744	22	AAK68361	Human immune/haema
33	214.4	40.1	13744	22	AAK82406	Human immune/haema
34	214	40.1	269	21	AAK06850	Human secreted pro
35	210.2	39.4	321	20	AAK97651	Extended human sec
36	205	38.4	207	24	ABN94246	Gene #744 used to
37	205	38.4	207	24	ABL62782	Breast cancer rela
38	205	38.4	207	24	ABL62959	Breast cancer rela
39	205	38.4	207	24	ABL63180	Breast cancer rela
40	201.4	37.7	326	24	ABO57138	Human colon cancer
41	185.2	34.7	495	20	AAK34052	Human EST DNA43509
42	185.2	34.7	495	21	AAK78499	Human EST DNA43509
43	185.2	34.7	495	22	AAK93358	CDNA encoding SRT
44	184.8	34.6	2953	22	AAK68359	Human immune/haema
45	184.8	34.6	2953	22	AAK68350	Human immune/haema

#### ALIGNMENTS

RESULT 1  
AAA38006 standard; CDNA; 534 BP.

XX AAA38006:  
XX  
XX  
XX 22-AUG-2000 (first entry)  
XX  
XX  
XX UCK-1 nucleotide sequence.  
XX  
XX  
XX UCK-1; chemotaxis factor; immunocyte; haemopoiesis stimulant; tumour;  
XX radiotherapy; chemotherapy; human; ss.  
XX  
XX Homo sapiens.  
XX  
XX CN1244584-A.  
XX  
XX 16-FEB-2000.  
XX  
XX 14-MAY-1999; 99CN-0107284.  
XX  
XX 14-MAY-1999; 99CN-0107284.  
XX  
XX 14-MAY-1999; 99CN-0107284.  
XX  
XX (UYBE-) UNIV BEIJING MEDICAL.  
XX  
XX Ma D, Han W, Zhang Y;  
XX  
XX WPI; 2000-388170/34.  
XX  
XX P-PSDB; AAY98142.  
XX  
XX Chemotactic factor useful for treatment and diagnosis of immunocyte  
XX disorders - has immunocyte chemotactic stimulating factor  
XX  
XX

XX Example 4; Fig 1; 31pp; Chinese.

CC This sequence represents an UCK-1 cDNA sequence encoding a chemotaxis  
CC factor polypeptide. The UCK-1 protein exhibits immunocyte chemotaxis  
CC activity and a haemopoiesis stimulating effect. The invention relates to  
CC UCK proteins, their encoding nucleotide sequences and antibodies and  
CC antagonists against the proteins. The nucleotide and protein sequences  
CC are useful for the preparation of a composition for the diagnosis and  
CC treatment of diseases associated with abnormal immunocyte function and  
CC low haemopoiesis function caused by radiotherapy and chemotherapy used to  
CC treat tumours and other diseases.

XX Sequence 534 BP; 156 A; 110 C; 134 G; 134 T; 0 other;

Query Match 100.0%; Score 534; DB 21; Length 534;  
Best Local Similarity 100.0%; Pred. No. 4.6e-107;  
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCCCAATCTGAAGTGAAGCCGAGCTGGCGAGAGTGAAGGGGCGGTCTCCGCG 60  
DB 1 GTTCCCAATCTGAAGTGAAGCCGAGCTGGCGAGAGTGAAGGGGCGGTCTCCGCG 60  
QY 61 CGGTGGCGGTCTCTATCGCTTGGCAACCTACTAGCAGCCAGCTGAGAGAGTTGAG 120  
DB 61 CGGTGGCGGTCTCTATCGCTTGGCAACCTACTAGCAGCCAGCTGAGAGAGTTGAG 120  
QY 121 GGAAGTGTCTGCTGGGTGCTGACAGCCGATGATTAAGCGAGCCGAAATTAACA 180  
DB 121 GGAAGTGTCTGCTGGGTGCTGACAGCCGATGATTAAGCGAGCCGAAATTAACA 180  
QY 181 TGGCCCTTCTCTCTCAGTGTGAAGCCGAGTGAAGTCTGCGGTGATATTATCA 240  
DB 181 TGGCCCTTCTCTCTCAGTGTGAAGCCGAGTGAAGTCTGCGGTGATATTATCA 240  
QY 241 CTCACGTGTAACACAGTATTCATGCTATCTGTTGGACAGATACCAAGAAC 300  
DB 241 CTCACGTGTAACACAGTATTCATGCTATCTGTTGGACAGATACCAAGAAC 300  
QY 301 CACAACATTTGACAGTGTGGAGGGGTTTGCACATTTGACAGCAGTATCTGCTTGC 360  
DB 301 CACAACATTTGACAGTGTGGAGGGGTTTGCACATTTGACAGCAGTATCTGCTTGC 360  
QY 361 GCACGGGGCCCTTATTTACCGAACCCTTGTCAATCCGACGGTCTTACCGAAGAA 420  
DB 361 GCACGGGGCCCTTATTTACCGAACCCTTGTCAATCCGACGGTCTTACCGAAGAA 420  
QY 421 GCGTGTGATGAAAAAAGAGTTTGTAAATTTATATCTTTTGTGATGATACAA 480  
DB 421 GCGTGTGATGAAAAAAGAGTTTGTAAATTTATATCTTTTGTGATGATACAA 480  
QY 481 GTATTAAACATATTTCTGTATTTCCAAAAAAGAGTTTGTAAATTTATATCTTTTGTGATGATACAA 534  
DB 481 GTATTAAACATATTTCTGTATTTCCAAAAAAGAGTTTGTAAATTTATATCTTTTGTGATGATACAA 534

RESULT 2  
AAS44932  
ID AAS44932 standard; cDNA; 655 BP.

AC AAS44932;  
XX  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE cDNA encoding novel human secretory protein, Seq ID No 13.  
XX  
XX  
KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;  
KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;  
KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;  
KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;  
KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;  
KW gut protection; lung; liver fibrosis; immune deficiency; infection;  
KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;

KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;  
KW fertility; analgesic; pain; antigen; ss.

OS Homo sapiens.

PN WO200166689-A2.

PD 13-SEP-2001.

PF 05-MAR-2001; 2001WO-US04942.

PR 07-MAR-2000; 2000US-0519705.

PR 19-MAY-2000; 2000US-0574454.

PR 17-JUN-2000; 2000US-0596193.

PR 14-JUL-2000; 2000US-0616847.

PR 19-SEP-2000; 2000US-0665363.

PR 20-OCT-2000; 2000US-0693267.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

DR WPI: 2001-589934/66.

DR P-PSDB: AAU28032.

PT Novel polypeptides and nucleic acids obtained from cDNA libraries

PT prepared from various human tissues, for diagnosis and treatment of

PT cancer, neurological, inflammatory, and autoimmune disorders -

XX Claim 1; SEQ ID No 13; 107pp; English.

XX The invention relates to novel isolated human secreted polypeptides (I)

XX and polynucleotides (II). (I) and (II) are useful for treating

XX inflammatory conditions such as arthritis, nephritis, Crohn's disease,

XX ischaemia-reperfusion injury, shock, sepsis, immune responses, and is

XX involved in increasing haematopoiesis, stem cell survival, bone growth

XX and remodeling. (I), (II) and modulators of (II) are useful for

XX prophylaxis or treatment of one or more cancers. (II) is also useful for

XX creating transgenic animals useful for studying the in vivo activities of

XX the polypeptide as well as for studying modulators of the polypeptides.

XX (I) induces the proliferation of neural cells and regeneration of nerve

XX and brain tissue and is useful for the treatment of central and

XX peripheral nervous system diseases and neuropathies, such as Alzheimer's,

XX Parkinson's disease, Huntington's disease, and amyotrophic lateral

XX sclerosis. In addition, (I) is involved in chemotactic or chemokinetic

XX activity, regulation of haematopoiesis and is useful for treating myeloid

XX or lymphoid cell disorders, platelet disorders such as thrombocytopenia

XX and for regeneration of bone, cartilage, tendon, ligament and/or nerve

XX tissue growth, and in tissue repair, healing of burns, incisions,

XX ulcers, for treating osteoporosis, osteoarthritis, bone degenerative

XX disorders, or periodontal disease. Furthermore, (I) is also useful for

XX gut protection or regeneration and treatment of lung or liver fibrosis,

XX reperfusion injury in various tissues, various immune deficiencies and

XX disorders including severe combined immunodeficiency (SCID), bacterial or

XX fungal infections, autoimmune disorders e.g. multiple sclerosis,

XX rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic

XX reactions and conditions, such as asthma or other respiratory problems.

XX In addition, (I) affects biorhythms or circadian cycles of rhythms,

XX fertility, metabolism, catabolism, anabolism, storage or elimination of

XX dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides

XX analgesic effects or other pain reducing effects, immunoglobulin like

XX activity and can act as an antigen in a vaccine composition to raise an

XX immune response. AAS44920-AAS45295 represent novel human secreted protein

XX coding sequences of the invention.

XX Sequence 655 BP; 178 A; 129 C; 181 G; 167 T; 0 other;

QY Query Match 94.9%; Score 507; DB 22; Length 655;  
Best Local Similarity 100.0%; Pred. No. 3.6e-101;  
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 AGCGAGCTGGCGGAGAGTGAAGGGGCGGTCTCCGCGCGGTGGCGGTCTGCTATCG 78



1 AGCCGAGCTGGGCGAAGATAGGGAGGGGCGGTGCTCCGGCGGGTGGCGGTTCATGCG 60

QY 79 CTTTCGAGAACCTACTACGAGCAGCCAGCTGGAAGAGTTGAAGGAAAGTCTGCTGCTGG 138

Dp 61 CTTTCGAGAACCTACTACGAGCAGCCAGCTGGAAGAGTTGAAGGAAAGTGTGTGCTGG 120

QY 139 GTCTCGAGACGGGATGAGTAACTGTCAGCCGCAAAATAAACATGCGCCCTTTCCTTCAG 198

Dp 121 GTCTCGAGACGGGATGAGTAACTGTCAGCCGCAAAATAAACATGCGCCCTTTCCTTCAG 180

QY 199 TGTGAAGAGCAGCGTAAGATGCTCGCGGTGGATTTATCACTCACTGGTAACACAGT 258

Dp 181 TGTGAAGAGCAGCGTAAGATGCTCGCGGTGGATTTATCACTCACTGGTAACACAGT 240

QY 259 ATTCACTCATCGTATCTGTGTGGCACTGATACAGAAACCAACATTTGACAGTTGG 318

Dp 241 ATTCACTCATCGTATCTGTGTGGCACTGATACAGAAACCAACATTTGACAGTTGG 300

QY 319 TGAAGGGGTGTGGCACTGTGACAGCAGTATGCTGTCTTCCGACGGGGCCCTTATTTA 378

Dp 301 TGAAGGGGTGTGGCACTGTGACAGCAGTATGCTGTCTTCCGACGGGGCCCTTATTTA 360

QY 379 CCGGAAGCTCTTTCATATCCAGGGGTCCTTACAGAAAAAGCCTGTCATGAAAAAA 438

Dp 361 CCGGAAGCTCTTTCATATCCAGGGGTCCTTACAGAAAAAGCCTGTCATGAAAAAA 420

QY 439 AGAAGTTTGTAAATTTATATATACATTTAGTTGATGATCAAGTATTAACATATTTCTG 498

Dp 421 AGAAGTTTGTAAATTTATATATACATTTAGTTGATGATCAAGTATTAACATATTTCTG 480

QY 499 TATTTCTCCAAAAAATTTTTTTTTT 525

Dp 481 TATTTCTCCAAAAAATTTTTTTTTT 507

RESULT 3	
AAH98515/C	
ID	AAH98515 standard; cDNA; 538 BP.
XX	
XX	
AC	AAH98515;
XX	
D7	12-OCT-2001 (first entry)
XX	
DE	Human EST-derived coding sequence SEQ ID NO: 372.
XX	
KW	Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW	tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW	diagnostics; forensic test; gene mapping; genetic disorder;
XX	biodiversity; gene therapy; nutrition; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200154477-A2.
XX	
PD	02-AUG-2001.
XX	
PF	25-JAN-2001; 2001WO-US02687.
XX	
PR	25-JAN-2000; 2000US-0491404.
PR	17-JUL-2000; 2000US-0617746.
PR	03-AUG-2000; 2000US-0631451.
PR	15-SEP-2000; 2000US-0663870.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI	Cao Y, Drmanac RA, Zhang J, Werhman T;
XX	
DR	WPI: 2001-476164/51.
DR	P-PSDB; AAM23856.
XX	
PT	Isolated polypeptide for treatment of diseases, diagnostics, raising

PT antibodies and research use -  
 XX  
 PS  
 XX  
 Claim 1; Page 451; 1275pp; English.  
 CC The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
 CC of the invention.  
 XX  
 SO Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;

Query Match	Similarity	93.3%	Score 498.2	DB 22	Length 538
Best Local	Similarity	99.4%	Pred No. 2.8e-99		
Matches 500	Conservative	0	Mismatches 3	Indels	Gaps 0
QY	15	GTGAAGCCGAGCTGGGCGAGAAATGAGGGAGGGCGGTCTCCCGCGGTGGCGTTC	74		
Db	503	GGGAGCCCGAGCTGGGCGAGAAATGAGGGAGGGCGGTCTCCCGCGGTGGCGTTC	444		
QY	75	ATGCGCTTCGAGAACTTACTACAGGACGACGTGAGAGAGTTGAGGGGAAAGTCTCTG	134		
Db	443	ATGCGCTTCGAGAACTTACTACAGGACGACGTGAGAGAGTTGAGGGGAAAGTCTCTG	384		
QY	135	CTGGGCTTCGAGACGGGATGATTAACGTGCACGCCGAAATTAACATCGCCCTTCGCT	194		
Db	383	CTGGGCTTCGAGACGGGATGATTAACGTGCACGCCGAAATTAACATCGCCCTTCGCT	324		
QY	195	TCAGTGTGAAGGCGACGAGAGATGCTGGCTGGATATTATCACTCACTGGTACAA	254		
Db	323	TCAGTGTGAAGGCGACGAGAGATGCTGGCTGGATATTATCACTCACTGGTACAA	264		
QY	255	CAGTATTCATGCATCATCGTATCTGTGTGGCACTGATACAGAAACCAACATTTGACAG	314		
Db	263	CAGTATTCATGCATCATCGTATCTGTGTGGCACTGATACAGAAACCAACATTTGACAG	204		
QY	315	TTGGTGTGAGGGGCTTTGCACTTGTGACAGCATGTATGCTGTTCGCGAGGGGCGCTTA	374		
Db	203	TTGGTGTGAGGGGCTTTGCACTTGTGACAGCATGTATGCTGTTCGCGAGGGGCGCTTA	144		
QY	375	TTTACCGGAGCTTCTGTTCAATCCACGCGGCTCTTACAGAAAAAGCCTGTGCATGAAA	434		
Db	143	TTTACCGGAGCTTCTGTTCAATCCACGCGGCTCTTACAGAAAAAGCCTGTGCATGAAA	84		
QY	435	AAAAAGAAAGTTTGTATATTTATATATCTTTTAAATGATATTAACATATT	494		
Db	83	AAAAAGAAAGTTTGTATATTTATATATCTTTTAAATGATATTAACATATT	24		
QY	495	TCTGTATTCTTCCAAAAA	517		
Db	23	TCTGTATTCTTAAAAA	1		
RESULT 4					
AAH98548/c					
ID	AAH98548 standard; cDNA; 538 BP.				
XX	AAH98548;				
XX	12-OCT-2001 (first entry)				
DT	Human EST-derived coding sequence SEQ ID NO: 405.				
DE	Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;				
XX	tomato; monkey; dog; sea urchin; expressed sequence tag; EST;				
KW	diagnostics; forensic test; gene mapping; genetic disorder;				
KX	biodiversity; gene therapy; nutrition; ss.				
OS	Homo sapiens.				
XX					

PN WO200154477-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 XX 25-JAN-2001; 2001WO-US02687.  
 PF  
 XX 25-JAN-2000; 2000US-0491404.  
 PR 17-JUL-2000; 2000US-0617746.  
 PR 03-AUG-2000; 2000US-0631451.  
 PR 15-SEP-2000; 2000US-0663870.  
 XX  
 PA (HSEF-) HSEBQ INC.  
 XX  
 XX Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 DR WPI; 2001-476164/51.  
 DR P-PSDB; AAM23889.  
 XX  
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use -  
 XX  
 PS Claim 1; Page 467; 1275pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a CDNA  
 CC of the invention.  
 XX  
 SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;  
 XX  
 Query Match 93.3%; Score 498.2; DB 22; Length 538;  
 Best Local Similarity 99.4%; Pred. No. 2.8e-99;  
 Matches 500; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 15 GTGAAGCCGAGCTGGGCGAGAGTAGGGAGGGGCTGCTCCGCGCGGTGGGCT 74  
 Db 503 GGGAGCCGAGCTGGGCGAGAGTAGGGAGGGGCTGCTCCGCGCGGTGGGCT 444  
 QY 75 ATCCGTTGGCAGAACCTTCTCAGCGCAGCCAGCTGAGAAAGTTGAGGAAAGTGGCTG 134  
 Db 443 ATCCGTTGGCAGAACCTTCTCAGCGCAGCCAGCTGAGAAAGTTGAGGAAAGTGGCTG 384  
 QY 135 CTGGGCTGCGAGACGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 194  
 Db 383 CTGGGCTGCGAGACGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 324  
 QY 195 TCAGTGTGAAGGCGCAGTGAAGATGCTGCGGCTGGATATTTATCACTGCTGTAACAA 254  
 Db 323 TCAGTGTGAAGGCGCAGTGAAGATGCTGCGGCTGGATATTTATCACTGCTGTAACAA 264  
 QY 255 CAGTATTCATCTCTATCTATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 314  
 Db 263 CAGTATTCATCTCTATCTATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 204  
 QY 315 TTGGTGAAGGCGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 374  
 Db 203 TTGGTGAAGGCGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 144  
 QY 375 TTTACCGGAGCTTCTGTTCAATCCAGCGGCTTACCAAGAAAGGCTGTGATGAAA 434  
 Db 143 TTTACCGGAGCTTCTGTTCAATCCAGCGGCTTACCAAGAAAGGCTGTGATGAAA 84  
 QY 435 AAAAGAGCTTTGTAATTTATATTTATTTATTTATTTATTTATTTATTTATTTATTT 494  
 Db 83 AAAAGAGCTTTGTAATTTATATTTATTTATTTATTTATTTATTTATTTATTTATTT 24  
 QY 495 TCTGATTCCTCCAAAAA 517  
 Db 495 TCTGATTCCTCCAAAAA 517

Db 23 TCTGATTCCTCCAAAAA 1  
 RESULT 5  
 ID AAH34835 standard; CDNA; 558 BP.  
 XX  
 XX AAH34835;  
 AC  
 XX 03-SEP-2001 (first entry)  
 DT  
 XX  
 XX Human colon cancer antigen encoding CDNA SEQ ID NO:1917.  
 DE  
 XX Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KW colorectal carcinoma; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 PN WO200122920-A2.  
 PD 05-APR-2001.  
 XX  
 XX 28-SEP-2000; 2000WO-US26524.  
 PF  
 XX 29-SEP-1999; 99US-0157137.  
 PR 03-NOV-1999; 99US-0163280.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
 DR WPI; 2001-235357/24.  
 DR P-PSDB; AAG75430.  
 XX  
 XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
 PT useful for preventing, diagnosing and/or treating colorectal cancers -  
 PT  
 XX  
 PS Claim 1; Page 3428; 9803pp; English.  
 XX  
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where  
 CC the proteins are collectively known as colon cancer antigens. The colon  
 CC cancer antigens have cytostatic activity and can be used in gene  
 CC therapy and vaccine production. N and P may be used in the prevention,  
 CC diagnosis and treatment of diseases associated with inappropriate P  
 CC expression. For example, N and P may be used to treat disorders  
 CC associated with decreased expression by rectifying mutations or deletions  
 CC in a patient's genome that affect the activity of P by expressing  
 CC inactive proteins or to supplement the patient's own production of P.  
 CC Additionally, N may be used to produce the colon cancer-associated Ps,  
 CC by inserting the nucleic acids into a host cell and culturing the cell  
 CC to express the proteins. N and P can be used in the prevention, diagnosis  
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204  
 CC and AAB77789 represent sequences used in the exemplification of the  
 CC present invention.  
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were  
 CC missing at time of publication, meaning no sequences are present for  
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.  
 XX  
 SQ Sequence 558 BP; 150 A; 119 C; 145 G; 141 T; 3 other;  
 XX  
 Query Match 93.1%; Score 497.2; DB 22; Length 558;  
 Best Local Similarity 98.4%; Pred. No. 4.7e-99;  
 Matches 499; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 16 TGAAGCGAGCTGGGCGAGAGTAGGGAGGGGCGGCTCCGCCGCGGGGCTTGCTA 75  
 Db 11 TGAAGTGGAGCTGGGCGAGAGTAGGGAGGGGCGGCTCCGCCGCGGGGCTTGCTA 70  
 QY 76 TCGCTTCGAGAACCTTCTCAGGCAAGCTGAGAGAGTGAAGGAAAGTGGCTGTC 135  
 Db 71 TCGCTTCGAGAACCTTCTCAGGCAAGCTGAGAGAGTGAAGGAAAGTGGCTGTC 130

OY 136 TGGGTCTGCAGACGCGATGATACGTCGACGCCGAAATATAACATGCGCCCTTCGCTT 195  
 DB 131 TGGGTCTGCAGACGCGATGATACGTCGACGCCGAAATATAACATGCGCCCTTCGCTT 190  
 OY 196 CAGGTGTAAGAGCCGACGTGAAGATGCTGCGCTGATATTTATCACTGCTGTAACAC 255  
 DB 191 CAGGTGTAAGAGCCGACGTGAAGATGCTGCGCTGATATTTATCACTGCTGTAACAC 250  
 OY 256 AGTATTCATGCTCATCTGATCTGTGTGGCAGCATGATCCGAAACCAACCATTTGACACT 315  
 DB 251 AGTATTCATGCTCATCTGATCTGTGTGGCAGCATGATCCGAAACCAACCATTTGACACT 310  
 OY 316 TGGGAGAGGGCTGTTTGCACCTTGACAGCAGTATGCTGCTTCCGACGGGGCCCTTAT 375  
 DB 311 TGGGAGAGGGCTGTTTGCACCTTGACAGCAGTATGCTGCTTCCGACGGGGCCCTTAT 370  
 OY 376 TTACCGGAAGCTTCTGTTCATTCGACGCGGTCTTTACAGAAAAAGCCTGTGCATGAAA 435  
 DB 371 TTACCGGAAGCTTCTGTTCATTCGACGCGGTCTTTACAGAAAAAGCCTGTGCATGAAA 430  
 OY 436 AAAAGAGCTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 495  
 DB 431 AAAAGAGCTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 490  
 OY 496 CTGTATTTCTTCCAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 522  
 DB 491 CTGTATTTCTTCCAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 517

RESULT 6  
 ID AAA87730 standard; cDNA; 515 BP.

AA87730:  
 28-NOV-2000 (first entry)  
 Human secreted protein encoding cDNA SEQ ID #29.

Human; secreted protein; forensic procedure; gene therapy;  
 chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;  
 cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;  
 brain disorder; skeletal muscle disorder; eye disorder; obesity;  
 mitochondrial cytochrome; diabetes; atherosclerosis; Alzheimer's disease;  
 neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;  
 septic shock; impotence; ss.

OS Homo sapiens.  
 PN WO200037491-A2.  
 PD 29-JUN-2000.  
 PF 20-DEC-1999; 99WO-IB02058.  
 PR 22-DEC-1998; 98US-0113686.  
 PR 25-JUN-1999; 99US-0141032.  
 PA (GENSET).

PI Bougueleret L, Dumas J, Duclert A;  
 DR WPI: 2000-442637/38.  
 DR P-PSDB: AAB25768.

PT Polynucleotides and polypeptides encoding proteins with signal  
 PT peptides, useful in diagnostic, forensic, gene therapy and chromosome  
 PT mapping procedures -

PS Claim 1, page 169-170; 306pp; English.

CC This sequence represents human cDNA encoding a secreted protein. The  
 CC invention relates to sequences AAA87725-A87774 which encode human

CC secreted proteins AAB25763-B25812. The proteins include signal peptides.  
 CC included in the invention are a host cell containing one of the cDNA  
 CC sequences, and a purified antibody capable of binding to one of the  
 CC secreted proteins. Also contained in the invention are methods for  
 CC storing the sequence data on a computer system, and a method for  
 CC identifying features of the cDNA sequences using a computer programme.  
 CC The cDNAs are useful for expressing secreted proteins or fragments to  
 CC obtain antibodies capable of specifically binding to the secreted  
 CC proteins. The cDNAs may also be useful in diagnostic, forensic, gene  
 CC therapy and chromosome mapping procedures and may be used to design  
 CC expression vectors and secretion vectors. The proteins of the invention  
 CC may be used to treat diseases including cancer, autoimmune diseases,  
 CC cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological  
 CC disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye  
 CC disorders, obesity, mitochondrial cytochromes, diabetes, atherosclerosis,  
 CC neurodegenerative disorders, graft rejection, Alzheimer's disease,  
 CC dementia, hyperlipidaemia, septic shock and impotence.

CC Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

Query Match 92.4%; Score 493.4; DB 21; Length 515;  
 Best Local Similarity 99.4%; Pred. No. 3.1e-98;  
 Matches 505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 15 GTGAGCCGAGCTGGCGAGAGTGAAGAGGAGGCGGTGCTCCGCGGCTGGCGGTGCT 74  
 DB 8 GGGAGCCGAGCTGGCGAGAGTGAAGAGGAGGCGGTGCTCCG -CGCGGTGGCNGTGT 66  
 OY 75 ATGCTTTCGACAGCTTACTCAGGCGAGCCAGCTGAGAAAGTTGAGGAGAAATGCTGCTG 134  
 DB 67 ATGCTTTCGACAGCTTACTCAGGCGAGCCAGCTGAGAAAGTTGAGGAGAAATGCTGCTG 126  
 OY 135 CTGGGTCTGCAGACGCGATGATACGTCGACGCCGAAATATAACATGCGCCCTTCGCT 194  
 DB 127 CTGGGTCTGCAGACGCGATGATACGTCGACGCCGAAATATAACATGCGCCCTTCGCT 186  
 OY 195 TCAAGTGAAGGCCAGCTGGAAGATGCTGGGTGATATTTATCACTGATGATGACAA 254  
 DB 187 TCAAGTGAAGGCCAGCTGGAAGATGCTGGGTGATATTTATCACTGATGATGACAA 246  
 OY 255 CAGTATTCATGCTCATACGATATCTGTGTCGATGATGATGATGATGATGATGATGATG 314  
 DB 247 CAGTATTCATGCTCATACGATATCTGTGTCGATGATGATGATGATGATGATGATGATG 306  
 OY 315 TTGGTGGAGGGGTTTGGCACTTGACAGCAGTATGCTGTTGGCGAGCGGGCCCTTA 374  
 DB 307 TTGGTGGAGGGGTTTGGCACTTGACAGCAGTATGCTGTTGGCGAGCGGGCCCTTA 366  
 OY 375 TTACCGGAAGCTTCTGTTCATTCGACGCGGTCTTTACAGAAAAAGCCTGTGCATGAAA 434  
 DB 367 TTACCGGAAGCTTCTGTTCATTCGACGCGGTCTTTACAGAAAAAGCCTGTGCATGAAA 426  
 OY 435 AAAAGAGCTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 494  
 DB 427 AAAAGAGCTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 486  
 OY 495 TGTGTATTTCTTCCAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 522  
 DB 487 TGTGTATTTCTTCCAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 514

RESULT 7  
 ID AAF64012 standard; cDNA; 515 BP.

AA64012:  
 05-APR-2001 (first entry)

CC cDNA encoding human secreted protein #13.

CC Secreted protein; prevention; treatment; diagnosis; disease;  
 CC infection; ds.

ID	AAV59598	standard; DNA; 504 bp.
XX		
AC	AAV59598;	
XX		
DT	06-JAN-1999	(first entry)
XX		
DE	Human secreted protein gene 88 clone HAAV32.	
XX		
KW	Human; secreted protein; fusion protein; gene therapy; protein therapy;	
KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;	
KW	developmental abnormality; foetal deficiency; blood; allergy; renal; ds;	
KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;	
KW	inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;	
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus	
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;	
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.	
XX		
OS	Homo sapiens.	
XX		
PN	W09839448-A2.	
XX		
PD	11-SEP-1998.	
XX		
PF	06-MAR-1998;	98WO-US04493.
XX		
PR	02-OCT-1997;	97US-0061060.
PR	07-MAR-1997;	97US-0038621.
PR	07-MAR-1997;	97US-0040161.
PR	07-MAR-1997;	97US-0040162.

OS	Homo sapiens.	
XX		
PN	W08393448-A2.	
XX		
PD	11-SEP-1998.	
PE	06-MAR-1998;	98W0-U504493
XX		
PR	02-OCT-1997;	97US-U061060
PR	07-MAR-1997;	97US-U038621
PR	07-MAR-1997;	97US-U0040161
PR	07-MAR-1997;	97US-U0040162
PR	07-MAR-1997;	97US-U0040163
PR	07-MAR-1997;	97US-U0040334
PR	07-MAR-1997;	97US-U0040336

RESULT 8  
AAV59598

ID	AAV59598 standard; DNA, 504 BP
XX	AAV59598;
AC	
XX	
DT	06-JAN-1999 (first entry)
XX	
DE	Human secreted protein gene 88
XX	
OS	Homo sapiens.
XX	
XX	MO839448-A2.
PN	
PD	11-SEP-1998.
XX	
PF	06-MAR-1998; 98WO-US04493.
XX	
XX	02-OCT-1997; 97US-0061060.
XX	07-MAR-1997; 97US-0038621.
PR	07-MAR-1997; 97US-0040161.
PR	07-MAR-1997; 97US-0040162.
PR	07-MAR-1997; 97US-0040163.
PR	07-MAR-1997; 97US-0040333.
PR	07-MAR-1997; 97US-0040334.
PR	07-MAR-1997; 97US-0040336.
PR	07-MAR-1997; 97US-0040311.
PR	11-APR-1997; 97US-0043312.
PR	11-APR-1997; 97US-0043313.
PR	11-APR-1997; 97US-0043314.
PR	11-APR-1997; 97US-0043368.
PR	11-APR-1997; 97US-0043369.
PR	11-APR-1997; 97US-0043376.
PR	11-APR-1997; 97US-0043378.
PR	11-APR-1997; 97US-0043659.
PR	11-APR-1997; 97US-0043670.
PR	11-APR-1997; 97US-0043672.
PR	11-APR-1997; 97US-0043674.
PR	23-MAY-1997; 97US-0047582.
PR	23-MAY-1997; 97US-0047583.
PR	23-MAY-1997; 97US-0047584.
PR	23-MAY-1997; 97US-0047585.
PR	23-MAY-1997; 97US-0047586.
PR	23-MAY-1997; 97US-0047587.
PR	23-MAY-1997; 97US-0047588.
PR	23-MAY-1997; 97US-0047589.
PR	23-MAY-1997; 97US-0047590.
PR	23-MAY-1997; 97US-0047591.
PR	23-MAY-1997; 97US-0047592.
PR	23-MAY-1997; 97US-0047593.
PR	23-MAY-1997; 97US-0047594.
PR	23-MAY-1997; 97US-0047595.
PR	23-MAY-1997; 97US-0047596.
PR	23-MAY-1997; 97US-0047597.
PR	23-MAY-1997; 97US-0047598.
PR	23-MAY-1997; 97US-0047599.
PR	23-MAY-1997; 97US-0047600.
PR	23-MAY-1997; 97US-0047601.

	PR	23-MAY-1997;	97US-0047612.
	PR	23-MAY-1997;	97US-0047613.
	PR	23-MAY-1997;	97US-0047614.
	PR	23-MAY-1997;	97US-0047615.
	PR	23-MAY-1997;	97US-0047617.
	PR	23-MAY-1997;	97US-0047618.
	PR	23-MAY-1997;	97US-0047632.
	PR	23-MAY-1997;	97US-0047633.
	PR	06-JUN-1997;	97US-0048964.
	PR	06-JUN-1997;	97US-0048974.
	PR	13-JUL-1997;	97US-0049610.
	PR	08-JUL-1997;	97US-0051926.
	PR	16-JUL-1997;	97US-0052874.
	PR	18-AUG-1997;	97US-0055724.
	PR	22-AUG-1997;	97US-0056630.
	PR	22-AUG-1997;	97US-0056631.
	PR	22-AUG-1997;	97US-0056632.
	PR	22-AUG-1997;	97US-0056636.
	PR	22-AUG-1997;	97US-0056637.
	PR	22-AUG-1997;	97US-0056662.
	PR	22-AUG-1997;	97US-0056664.
	PR	22-AUG-1997;	97US-0056685.
	PR	22-AUG-1997;	97US-0056686.
	PR	22-AUG-1997;	97US-0056864.
	PR	22-AUG-1997;	97US-0056872.
	PR	22-AUG-1997;	97US-0056874.
	PR	22-AUG-1997;	97US-0056875.
	PR	22-AUG-1997;	97US-0056876.
	PR	22-AUG-1997;	97US-0056877.
	PR	22-AUG-1997;	97US-0056878.
	PR	22-AUG-1997;	97US-0056879.
	PR	22-AUG-1997;	97US-0056880.
	PR	22-AUG-1997;	97US-0056881.
	PR	22-AUG-1997;	97US-0056882.
	PR	22-AUG-1997;	97US-0056884.
	PR	22-AUG-1997;	97US-0056886.
	PR	22-AUG-1997;	97US-0056887.
	PR	22-AUG-1997;	97US-0056889.
	PR	22-AUG-1997;	97US-0056892.
	PR	22-AUG-1997;	97US-0056893.
	PR	22-AUG-1997;	97US-0056894.
	PR	22-AUG-1997;	97US-0056903.
	PR	22-AUG-1997;	97US-0056908.
	PR	22-AUG-1997;	97US-0056909.
	PR	22-AUG-1997;	97US-0056910.
	PR	05-SEP-1997;	97US-0057650.
	PR	05-SEP-1997;	97US-0057669.
	PR	05-SEP-1997;	97US-0057761.
	PR	12-SEP-1997;	97US-0058785.
	XX		
	PA	(HUMA-) HUMAN GENOME SCI INC.	
	XX		
	PB	Bednarik DP, Brewer LA, Carter KC, Duan R, Ebnur R, Endress GA; Feng P, Ferlie AM, Fischer CL, Florence KA, Greene JW, Hu JS, Kyam H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z.  WPI; 1998-506364/43. P-PSTDB; AAW74818.	
	DR		
	XX		
	PT	New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders	
	PS	Claim 1; Page 320; 72ip; English.	
	XX		
	CC	This sequence represents a nucleic acid molecule designated Gene 88 from the human cDNA clone HANAV32 (deposited as clone ATCC 97901 and ATCC 209047) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of	
	CC		

Query Match	91.1%;	Score 486.6;	DB 19;	Length 504;
Best Local Similarity	99.0%;	Pred. No. 9,4e-97;		
Matches 500;	Conservative 0;	Mismatches 4;	Indels 1;	Gaps 1
CC	the fused protein as compared to the human protein only.			
CC	CC The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)			
CC	CC which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for described uses).			
XX	Sequence 504 BP; 143 A; 106 C; 128 G; 127 T; 0 other;			
QY	21 CCAGAGCTGGGCCGAGAAAGTACGGGAGGGCGGTCTCCCGCGGGGGGGTGGTACGCT 80			
Db	1 CCGAGCTGGGGCGGAAAGTACGGGAGGGGCG-ACGAGCGCGGGGGGCGGTGGTACGCT 59			
QY	81 TCCGACAGACCTACTCTACGAGCGACGACGTGAGAAAGATTGAGGAAAGTGTCTGCTGGGT 140			
Db	60 TCCGACAGACCTACTCTACGAGCGACGACGTGAGAAAGATTGAGGAAAGTGTCTGCTGGGT 119			
QY	141 CTGCACAGCGAGTATGATTAACCTGTGCACGCCGAAATTAACATCGCCCTCTCTTCAGTG 200			
Db	120 CTGCACAGCGAGTATGATTAACCTGTGCACGCCGAAATTAACATCGCCCTCTCTTCAGTG 179			
QY	201 TGAAGAGCCAGCGTGAAGATGTGCGGCTGGATATTATCACTCACTGGTAAACAGATAT 260			
Db	180 TGAAGAGCCAGCGTGAAGATGTGCGGCTGGATATTATCACTCACTGGTAAACAGATAT 239			
QY	261 TCATGCTCATCTGATCTGTGTGGCAGCTGATACCGAAGAACCAACATTTGACATTTGCTG 320			
Db	240 TCATGCTCATCTGATCTGTGTGGCAGCTGATACCGAAGAACCAACATTTGACATTTGCTG 299			
QY	321 GAGGGGGTGTGGACCTGTGACAGCAGTATGCTGCTTGGCGAGCGGGGCCCTTATTAC 380			
Db	300 GAGGGGGTGTGGACCTGTGACAGCAGTATGCTGCTTGGCGAGCGGGGCCCTTATTAC 359			
QY	381 GGAAGCTTGTTCATCCGAGCGTCTTACCCAGAAAGAGCCCTGTGATAAAAAAG 440			
Db	360 GGAAGCTTGTTCATCCGAGCGTCTTACCCAGAAAGAGCCCTGTGATAAAAAAG 419			
QY	441 AAGTTTGTAAATTTATATCTTAACTTTGATGATTAAGTATTAACATATTCTGTA 500			
Db	420 AAGTTTGTAAATTTATATCTTAACTTTGATGATTAAGTATTAACATATTCTGTA 479			
QY	501 TTCTTCCAAAAAAGAAAAAAG 525			
Db	480 TTCTTCCAAAAAAGAAAAAAG 504			
RESULT 9				
AAV59746				
ID	AAV59746 standard; DNA; 506 BP.			
XX	AAV59746;			
XX	19-JAN-1999 (first entry)			
DE	Human secreted protein gene 88 clone HAUWV32.			
XX	Human: secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.			

```

OS Homo sapiens.
XX
XX MO9839448-A2.
XX
PD 11-SEP-1998.
XX
XX 06-MAR-1998; 98MO-US04493.
XX
PR 02-OCT-1997; 97US-0061060.
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040626.
PR 11-APR-1997; 97US-0043311.
PR 11-APR-1997; 97US-0043312.
PR 11-APR-1997; 97US-0043313.
PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043566.
PR 11-APR-1997; 97US-0043569.
PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043669.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043677.
PR 23-MAY-1997; 97US-0043678.
PR 23-MAY-1997; 97US-0043679.
PR 23-MAY-1997; 97US-0043700.
PR 23-MAY-1997; 97US-0043701.
PR 23-MAY-1997; 97US-0043702.
PR 23-MAY-1997; 97US-0043703.
PR 23-MAY-1997; 97US-0047581.
PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047583.
PR 23-MAY-1997; 97US-0047584.
PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048964.
PR 13-JUN-1997; 97US-0049610.
PR 08-JUL-1997; 97US-0051926.
PR 16-JUL-1997; 97US-0052874.
PR 18-AUG-1997; 97US-0055724.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
PR 22-AUG-1997; 97US-0056632.
PR 22-AUG-1997; 97US-0056636.
PR 22-AUG-1997; 97US-0056637.
PR 22-AUG-1997; 97US-0056662.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056665.
PR 22-AUG-1997; 97US-0056682.
PR 22-AUG-1997; 97US-0056684.
PR 22-AUG-1997; 97US-0056687.
PR 22-AUG-1997; 97US-0056688.
PR 22-AUG-1997; 97US-0056689.
PR 22-AUG-1997; 97US-0056690.
PR 22-AUG-1997; 97US-0056691.
PR 22-AUG-1997; 97US-0056692.
PR 22-AUG-1997; 97US-0056693.
PR 22-AUG-1997; 97US-0056694.
PR 22-AUG-1997; 97US-0056698.
PR 22-AUG-1997; 97US-0056708.
PR 22-AUG-1997; 97US-0056808.
PR 22-AUG-1997; 97US-0056809.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057659.
PR 05-SEP-1997; 97US-0057761.
PR 12-SEP-1997; 97US-0058785.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA,
XX Feng P, Ferris AM, Fischer CL, Florence KA, Greene JM, Hu JS,
XX Kraw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,
XX Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX WPI; 1998-506364/43.
XX P-PSDB; AAW74961.
XX
XX New isolated human genes and the secreted polypeptide(s) they encode
XX - useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 1; Page 472; 721pp; English.
XX
XX This sequence represents a nucleic acid molecule designated Gene 88 from
XX the human cDNA clone HANA923 (deposited as clone ATCC 97897 and ATCC
XX 209043) which encodes a secreted human protein. The gene can be used to
XX generate fusion proteins by linking to the gene to a human
XX immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
XX the fused protein as compared to the human protein only.
XX CC The invention relates to 186 novel genes and their fragments (nucleic
XX acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)
XX which are useful for preventing, treating or ameliorating medical
XX conditions e.g. by protein or gene therapy. Also, pathological
XX conditions can be diagnosed by determining the amount of the new
XX polypeptides in a sample or by determining the presence of mutations in
XX the new polynucleotides. Specific uses are described for each of the 186
XX polynucleotides, based on which tissues they are most highly expressed in
XX (see AAV59511 for described uses).
XX
XX Sequence 506 BP; 148 A; 103 C; 121 G; 132 T; 2 other;
XX
XX Query Match 89.6%; Score 478.6; DB 19; Length 506;
XX Best Local Similarity 97.4%; Pred. No. 5.2e-95;
XX Matches 484; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

```

QY	37	GTAGAGGGAAGGGGAGTCCCGCCGGGGGGGGTTCATCGCTTCGCAACCTACTCA	96
	1		111
	2	GCAGGATTTGGCCAGGACCCGCCCGGGGTGGCTATCGCTTCGCACAACTACTCA	61
Db	2		
QY	97	GGCAGCCAGCTGAGAAAGATTGAGGGAAGTGTGCTGTCTGTGGTCTGCAGACGGGATGGA	156
	1		111
	2	GGCAGCCAGCTGAGAAAGATTGAGGGAAGTGTGCTGTGGTCTGCAGACGGGATGGA	121
Db	62		
QY	157	TAACTGTGACGGCGGAAATATAAATCATCGGCCCTTCGCTTCAGTGTGGAAGGCCACGGAA	216
	1		111
	2	TAACTGTGACGGCGGAAATATAAATCATCGGCCCTTCGCTTCAGTGTGGAAGGCCACGGAA	181
Db	122		
QY	217	GATGCTGGCGCTGGATTTATTCACCTACTGCTAACCAACAGTATTCATGCTCATCGTATC	276
	1		111
	2	GATGCTGGCGCTGGATTTATTCACCTACTGCTAACCAACAGTATTCATGCTCATCGTATC	241
Db	182		
QY	277	TGTGTTGGGACATGATATCCAGAAACCAACAACATGTGACATGGGTGGAGGGGTGTGGACT	336
	1		111
	2	TGTGTTGGGACATGATATCCAGAAACCAACAACATGTGACATGGGTGGAGGGGTGTGGACT	301
Db	242		
QY	337	TGTGACAGCAGTATGCTGTCTTGCAGCGAGGGGCCCTTATTTACCGGAAAGCTTCTGTTCAA	396
	1		111
	2	TGTGACAGCAGTATGCTGTCTTGCAGCGAGGGGCCCTTATTTACCGGAAAGCTTCTGTTCAA	361
Db	302		
QY	397	TCCACACGGCTTACACAAAAACCTGTGATGAATAAAAAAGAAAGTTTGTGAATTTTA	456
	1		111
	2	TCCACACGGCTTACACAAAAACCTGTGATGAATAAAAAAGAAAGTTTGTGAATTTTA	421
Db	362		
QY	457	TATTACTTTTACTTTGATACTAAGTATTTAAACATATTTCTGTATTTCTTCCAAAAAAA	516
	1		111
	2	TATTACTTTTACTTTGATACTAAGTATTTAAACATATTTCTGTATTTCTTCCAAAAAAA	481
Db	422		
QY	517	AAAAAAAAAAAAAAAA 533	
	1		111
	2	AAAAAAAAAAAAAAAA 498	
Db	482		

Accession	Source	Accession	Source	Accession	Source	Accession	Source
AA97826	standard; cDNA; 500 BP.	AA97826	standard; cDNA; 500 BP.	AA97826	standard; cDNA; 500 BP.	AA97826	standard; cDNA; 500 BP.
AA97826		AA97826		AA97826		AA97826	
23-SEP-1999	(first entry)	23-SEP-1999	(first entry)	23-SEP-1999	(first entry)	23-SEP-1999	(first entry)
Human secreted protein encoding cDNA #14.		Human secreted protein encoding cDNA #14.		Human secreted protein encoding cDNA #14.		Human secreted protein encoding cDNA #14.	
Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;		Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;		Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;		Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;	
diagnostic; gene therapy; chromosome mapping; secretion vector; ss.		diagnostic; gene therapy; chromosome mapping; secretion vector; ss.		diagnostic; gene therapy; chromosome mapping; secretion vector; ss.		diagnostic; gene therapy; chromosome mapping; secretion vector; ss.	
Homo sapiens.		Homo sapiens.		Homo sapiens.		Homo sapiens.	
W09925825-A2.		W09925825-A2.		W09925825-A2.		W09925825-A2.	
27-MAY-1999.		27-MAY-1999.		27-MAY-1999.		27-MAY-1999.	
13-NOV-1998; 98WO-IB01862.		13-NOV-1998; 98WO-IB01862.		13-NOV-1998; 98WO-IB01862.		13-NOV-1998; 98WO-IB01862.	
04-SEP-1998; 98US-0092973.		04-SEP-1998; 98US-0092973.		04-SEP-1998; 98US-0092973.		04-SEP-1998; 98US-0092973.	
13-NOV-1997; 97US-0066577.		13-NOV-1997; 97US-0066577.		13-NOV-1997; 97US-0066577.		13-NOV-1997; 97US-0066577.	
17-DEC-1997; 97US-0069957.		17-DEC-1997; 97US-0069957.		17-DEC-1997; 97US-0069957.		17-DEC-1997; 97US-0069957.	
09-FEB-1998; 98US-0074121.		09-FEB-1998; 98US-0074121.		09-FEB-1998; 98US-0074121.		09-FEB-1998; 98US-0074121.	
13-APR-1998; 98US-0081563.		13-APR-1998; 98US-0081563.		13-APR-1998; 98US-0081563.		13-APR-1998; 98US-0081563.	
10-AUG-1998; 98US-0096116.		10-AUG-1998; 98US-0096116.		10-AUG-1998; 98US-0096116.		10-AUG-1998; 98US-0096116.	
(GIST ) GENSET.		(GIST ) GENSET.		(GIST ) GENSET.		(GIST ) GENSET.	
Bougueleret L, Duclert A, Dumas Milne Edwards J;		Bougueleret L, Duclert A, Dumas Milne Edwards J;		Bougueleret L, Duclert A, Dumas Milne Edwards J;		Bougueleret L, Duclert A, Dumas Milne Edwards J;	
WPI; 1999-347472/29.		WPI; 1999-347472/29.		WPI; 1999-347472/29.		WPI; 1999-347472/29.	
P-PSDB; AAY36142.		P-PSDB; AAY36142.		P-PSDB; AAY36142.		P-PSDB; AAY36142.	
Extended cDNAs encoding secreted proteins		Extended cDNAs encoding secreted proteins		Extended cDNAs encoding secreted proteins		Extended cDNAs encoding secreted proteins	

xx Example 28; Page 173-174; 307pp; English.  
ps  
xx  
cc AAY97813-789706 represent extended cDNA's which encode novel human  
cc secreted proteins (see AAY6129-736222) and which have cytostatic,  
cc thrombotic and osteopathic activity. The extended cDNAs can be used to  
cc express secreted proteins or parts of them or to obtain antibodies  
cc capable of binding to the secreted proteins. They may also be used in  
cc diagnostic, forensic, gene therapy and chromosome mapping procedures.  
cc Uses also include design of expression vectors and secretion vectors.  
xx  
SQ Sequence 500 BP; 135 A; 102 C; 125 G; 129 T; 9 other;

Query Match	Similarity	97.4%	Score 466.8	DB 20	Length 500
Best Local	Similarity	97.8%	Pred. No. 1.9e-92		
Matches	Conservative	4	Mismatches	5	Indels
					Gaps
QY	23	GAGCTGGGCGAAGAACTAGGGGAGGGCGGTCTCCGCCCGCGTGCGG- TTGCTATCGCTT	81		
DB	2	GAGCTGTNNCNSAAGTAGGGGAGGGCGGCGTCCCGCMGCGTGGCGGHTGCTATCGCTT	61		
QY	82	CGCAAAACCTACTCAGCGACCGACGTGAGAAAGTTGAGGGGAAAGTGGCGTGGGGGTC	141		
DB	62	CGCAAAACCTACTCAGCGACCGACGTGAGAAAGTTGAGGGGAAAGTGGCGTGGGGTC	121		
QY	142	TGCAGACGCGATGATGATTAACGTGACACCGCAAAATTAACATCGCCCTTCTGCTCAGTGT	201		
DB	122	TGCAGACGCGATGATGATTAACGTGACACCGCAAAATTAACATCGCCCTTCTGCTCAGTGT	181		
QY	202	GAAAGGCGACGTGA-AGATGCTGGCGGCTGGATATTATCACTCAGTGGTAAACAAGTAT	260		
DB	182	GAAAGGCGACGTGAAGATGCTGGCGGCTGGATATTATCACTCAGTGGTAAACAAGTAT	241		
QY	261	TCATGCTCATGCTATCTGTTGGGACACTGATACCAAGAACCAACATGAGACGTGGTG	320		
DB	242	TCATGCTCATGCTATCTGTTGGGACACTGATACCAAGAACCAACATGAGACGTGGTG	301		
QY	321	GAGGGGTGTTTTCACATTGTGACAGCAGTATGCTGTTCCGACGAGGGGCCCTTATTACC	380		
DB	302	GAGGGGTGTTTTCACATTGTGACAGCAGTATGCTGTTCCGACGAGGGGCCCTTATTACC	361		
QY	381	GGAAGCTTCTGTTCAATCCCGACGCGTCTTACAGAAAAAGCTGTGCATGAAAAAAAAG	440		
DB	362	GGAAGCTTCTGTTCAATCCCGACGCGTCTTACAGAAAAAGCTGTGCATGAAAAAAAAG	421		
QY	441	AAGTTTGTAAATTTTATTTACTTTTACTTTGATGATCTAAGTATTAACATATTTCTGTA	500		
DB	422	AAGTTTGTAAATTTTATTTACTTTTACTTTGATGATCTAAGTATTAACATATTTCTGTA	481		
QY	501	TTCTTCCAAAAAAGAAAAA 519			
DB	482	TTCTTCCAAAAAAGAAAAA 500			
RESULT 11					
AAA15929	ID	AAA15929 standard; cDNA; 467 BP.			
XX	AA15929;				
XX	12-JUN-2000	(first entry)			
DE		Human protein clone HP10357 full length coding sequence.			
XX		Human protein: hydrophobic domain; nutritional source; haematopoiesis;			
KW		cytokine production; cell proliferation; cell differentiation;			
KW		immune deficiency; infectious disease; autoimmune disorder; asthma;			
KW		multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;			
KW		allergic reaction; osteoporosis; osteoarthritis; periodontal disease;			
KW		nervous system disorder; Alzheimer's disease; Parkinson's disease;			
KW		Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;			
KW		systemic cytokine damage; tissue differentiation; contraceptive; stroke;			
KW		coagulation disorder; myocardial infarction; inflammatory condition;			

KM septic shock; sepsis; ischaemia, reperfusion injury; arthritis; tumour;  
 KM nephritis; therapy; ss.  
 XX  
 OS Homo sapiens.  
 PN WO200005367-A2.  
 PN 03-FEB-2000.  
 PD  
 PD 22-JUL-1999; 99MO-JP03929.  
 PF  
 PR 24-JUL-1998; 98JP-0208820.  
 PR 07-AUG-1998; 98JP-0224105.  
 PR 25-AUG-1998; 98JP-0238116.  
 PR 09-SEP-1998; 98JP-0254736.  
 PR 29-SEP-1998; 98JP-0275505.  
 XX  
 PA (SAGA ) SAGAMI CHEM RES CENT.  
 PA (PROT-) PROTEGENE INC.  
 XX  
 XX Kato S, Kimura T;  
 XX  
 DR WPI: 2000-182694/16.  
 DR P-PSDB: AAY94861.  
 XX  
 PT Novel human proteins having hydrophobic domains useful for treating  
 PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,  
 PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -  
 PS Claim 4; Page 228; 351pp; English.  
 XX  
 CC This sequence encodes a human protein of the invention, which has  
 CC hydrophobic domains. The DNA sequences can be used as a probe or as a  
 CC genetic marker. The protein can also be used as a marker, and to identify  
 CC potential genetic disorders. The DNA and protein can also be used as  
 CC nutritional sources or supplements. The protein exhibits cytokine, cell  
 CC proliferation, cell differentiation activities and induces production of  
 CC other cytokines in certain cell populations. The protein also exhibits  
 CC immune stimulating or immune suppressing activity. It can be used in the  
 CC treatment of various immune deficiencies and disorders, and to treat  
 CC infectious diseases caused by viral, bacterial, fungal or other  
 CC infections. The protein is also used for treating autoimmune disorders  
 CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid  
 CC arthritis. It is also useful in the treatment of allergic reactions and  
 CC conditions such as asthma, and in immune suppression after organ  
 CC transplantation. The protein is useful in regulation of haematopoiesis  
 CC and consequently in the treatment of myeloid or lymphoid cell  
 CC deficiencies. It is also used in compositions for tissue growth or  
 CC regeneration. The protein is also used in the treatment of osteoporosis  
 CC or osteoarthritis and in the treatment of periodontal disease and other  
 CC tooth repair processes. The protein is used in the treatment of nervous  
 CC system disorders such as Alzheimer's disease, Parkinson's disease, and  
 CC Huntington's disease. They are useful for protection or regeneration and  
 CC treatment of lung or liver fibrosis, reperfusion injury in various  
 CC tissues, and conditions resulting from systemic cytokine damage. They are  
 CC also used for promoting or inhibiting tissue differentiation. They are  
 CC also used as contraceptives since they exhibit activin or inhibin related  
 CC activities and as a fertility inducing therapeutic. They are used for  
 CC treating various coagulation disorders and in treatment and prevention of  
 CC conditions resulting from coagulation activities e.g. myocardial  
 CC infarction or stroke. They also acts as receptors, receptor ligands or  
 CC inhibitors or agonists of receptor/ligand interactions. They are used to  
 CC treat inflammatory conditions such as septic shock, sepsis, ischaemia  
 CC reperfusion injury, arthritis, and nephritis. They can be used to  
 CC prevent tumours.  
 CC  
 CC Sequence 467 BP; 118 A; 101 C; 121 G; 127 T; 0 other;  
 XX  
 Query Match 87.2%; Score 465.4; DB 21; Length 467;  
 Best Local Similarity 99.8%; Pred. No. 3.8e-92;  
 Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0  
 39 AGGGGAGGCGGTGCTCCGCGCGGTGGCGTGTCTGATACGCTTCGAGACCTACTACAGG 98

Db	1	AGGGGAGGGCGGTCTCTCCGCCGGGTGGCCGGTTGCTATGCTTCCGAGAACCCTACTCAGG	60
QY	99	CAGCCAGCTGGAAGAGTTGAGGGGAAGTGTCTGCTGCTGGTCTGTGAGACGGGATGATA	15
Db	61	CAGCCAGCTGGAAGAGTTGAGGGGAAGTGTCTGCTGCTGGTCTGTGAGACGGGATGATA	120
QY	159	ACGTGCACCCGAAAAATAAAAATCATGCCCTTCTGCTTCAGTGTGAAGGCCACGTGAGA	210
Db	121	ACGTGCAGCCGAAAAATAAAAATCATGCCCTTCTGCTTCAGTGTGAAGGCCACGTGAGA	180
QY	219	TGCTGGCGGCTGGATATATATCACTCACTGGTAACAACTATTCATGCTCATGTAATCTG	270
Db	181	TGCTGGCGGCTGGATATATATCACTCACTGGTAACAACTATTCATGCTCATGTAATCTG	240
QY	279	TGTTGGCAGTGAATACCAAGAACCAACATTCAGTGTGGAGGGGTTGTGCATTG	330
Db	241	TGTTGGCAGTGAATACCAAGAACCAACATTCAGTGTGGAGGGGTTGTGCATTG	300
QY	339	TGACAGCAGTATGCTGTCTTGGCCGAGGGGCCCTTATTTACCGGAAGCTTGTGTCATTC	390
Db	301	TGACAGCAGTATGCTGTCTTGGCCGAGGGGCCCTTATTTACCGGAAGCTTGTGTCATTC	360
QY	399	CCACGGGCGCTTACCAAGAAAAAGCCGTGCATGAAAAAAGAAAGTTTGTAAATTTATA	450
Db	361	CCACGGGCTCTTACCAAGAAAAAGCCGTGCATGAAAAAAGAAAGTTTGTAAATTTATA	420
QY	459	TTACTTTTATGTTGATTAAGTAAATTAACAATTTCTGTAATCTT	505
Db	421	TTACTTTTATGTTGATTAAGTAAATTAACAATTTCTGTAATCTT	467

RESULT 12

ABK36006

ABK36006 standard; cDNA: 439 BP.

XX AC ABR36006;

XX DT 08-MAY-2002 (first entry)

DE cdna sequence #397 encoding novel human secreted protein.

KW Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; allergic condition; neurodegenerative disorder; liver fibrosis; coagulation disorder; gene therapy; antimicrobial; tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.

XX OS Homo sapiens.

XX PN WO200177289-A2.

XX PD 18-OCT-2001.

XX PF 29-MAR-2001; 2001WO-US10232.

XX PR 06-APR-2000; 2000US-195605P.

XX PA (GEMT.) GENETICS INST INC.

PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C, Meberg D, Tracy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG, Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR; WPI; 2002-179322/23.

XX six hundred and twenty three polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders

XX Claim 1; Page 296-297; 393pp; English.



CC The present invention relates to the isolation of novel cDNA sequences  
 CC which encode human secreted proteins. The cDNA sequences have been  
 CC derived from a variety of human tissues. The invention also provides  
 CC a method for producing proteins from these polynucleotide sequences.  
 CC The proteins are useful for identifying compounds that modulate their  
 CC activity and production. The sequences of the invention are  
 CC useful for treating diseases such as hyperproliferative disorders  
 CC (e.g. cancer), immune deficiency disorders (e.g. severe combined  
 CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple  
 CC sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory  
 CC disorders (e.g. arthritis), infectious disorders (e.g. hepatitis),  
 CC allergic conditions (e.g. asthma), neurodegenerative disorders (e.g.  
 CC Alzheimer's disease), liver fibrosis, coagulation disorders (e.g.  
 CC haemophilia), and tumours. The polynucleotide sequences of the  
 CC invention are also useful in gene therapy. ABK35610-ABK36232 represent  
 CC the cDNA sequences of the invention that encode for novel human  
 CC secreted proteins.

XX Sequence 439 BP; 117 A; 96 C; 104 G; 122 T; 0 other;

Query Match 79.6%; Score 425; DB 24; Length 439;

Best Local Similarity 99.8%; Pred. No. 2.3e-83; Mismatches 436; Conservative 0; Indels 1; Gaps 1;

DB 72 GGTATCGCTGGCAAGACCTACTGAGGAGCGAGCTGAGAGAGTGAAGGAAAGTGTG 131  
 1 GGTATCGCTGGCAAGACCTACTGAGGAGCGAGCTGAGAGAGTGAAGGAAAGTGTG 60  
 OY 132 CTGCTGGGTCTGCAGACGCGATGATTAACGTCAGCCGAAATTAACATCGCCCTTCT 191  
 DB 61 CTGCTGGGTCTGCAGACGCGATGATTAACGTCAGCCGAAATTAACATCGCCCTTCT 120  
 OY 132 GCTTACGTGTGAAGAGCCACGTAAGATGCTGGCTGATTTTCAACACACGTA 251  
 DB 121 GCTTACGTGTGAAGAGCCACGTAAGATGCTGGCTGATTTTCAACACACGTA 180  
 OY 252 CAACAGTATTCATGCTCATGCTGATGCTGGTGGACACTGATTAACAGCAATTTGA 311  
 DB 181 CAACAGTATTCATGCTCATGCTGATGCTGGTGGACACTGATTAACAGCAATTTGA 240  
 OY 312 CAGTTGGTGGAGGGGTGTTGCACTGTGACAGCAATGCTGTCCGACGGGGCC 371  
 DB 241 CAGTTGGTGGAGGGGTGTTGCACTGTGACAGCAATGCTGTCCGACGGGGCC 300  
 OY 372 TTAATTACCGGAAGCTTCTGTTCAATCCACGGGCTTACAGAAAAGCCTGTCATG 431  
 DB 301 TTAATTACCGGAAGCTTCTGTTCAATCCACGGGCTTACAGAAAAGCCTGTCATG 360  
 OY 432 AAAAAAAGAGTGTGTAATTTTATTTACTTTTATTTAGTTT-GATACATAAGTAAACA 490  
 DB 361 AAAAAAAGAGTGTGTAATTTTATTTACTTTTATTTAGTTTGGATACATAAGTAAACA 420  
 OY 491 TATTTCTGTATTTCTTC 507  
 DB 421 TATTTCTGTATTTCTTC 437

RESULT 13  
 AAX97873  
 ID AAX97873 standard; cDNA; 413 BP.

XX AAX97873;  
 XX  
 XX 23-SEP-1999 (first entry)  
 DE Human secreted protein encoding cDNA #61.  
 XX  
 XX Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;  
 KM diagnostic; gene therapy; chromosome mapping; secretion vector; ss.  
 OS Homo sapiens.  
 XX  
 XX WO925825-A2.  
 PN

XX 27-MAY-1999.  
 PD  
 XX 13-NOV-1998; 98WO-IB01862.  
 PF  
 XX 04-SEP-1998; 98US-0099273.  
 PR 13-NOV-1997; 97US-0066677.  
 PR 17-DEC-1997; 97US-0069957.  
 PR 09-FEB-1998; 98US-0074121.  
 PR 13-APR-1998; 98US-0081563.  
 PR 10-AUG-1998; 98US-0096116.  
 PA (GSEST ) GENSET.  
 XX  
 XX Bougueleret L, Duclert A, Dumas Milne Edwards J;  
 PI WPI: 1999-347472/29.  
 DR P-PSDB; AAY36189.  
 DR  
 XX Extended cDNAs encoding secreted proteins

XX Claim 1; Page 261; 307pp; English.

CC AAX97813-X97906 represent extended cDNA's which encode novel human  
 CC secreted proteins (see AAY36129-Y36222) and which have cytosolic,  
 CC thrombotic and osteopathic activity. The extended cDNAs can be used to  
 CC express secreted proteins or parts of them or to obtain antibodies  
 CC capable of binding to the secreted proteins. They may also be used in  
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 CC Uses also include design of expression vectors and secretion vectors.

XX Sequence 413 BP; 121 A; 82 C; 95 G; 115 T; 0 other;

Query Match 77.0%; Score 411.4; DB 20; Length 413;

Best Local Similarity 99.8%; Pred. No. 2.1e-80; Mismatches 412; Conservative 0; Indels 1; Gaps 0;

DB 107 TGAGAAAGTGTGAGGAAAGTGTGCTGCTGGGTCTGCAGACGCGATGATTAACGTCAG 166  
 1 TGAGAAAGTGTGAGGAAAGTGTGCTGCTGGGTCTGCAGACGCGATGATTAACGTCAG 60  
 OY 167 CCGAAATTAACATCGCCCTTCTGCTTGAAGTGAAGCCACGTAAGATGCTGCGG 226  
 DB 61 CCGAAATTAACATCGCCCTTCTGCTTGAAGTGAAGCCACGTAAGATGCTGCGG 120  
 OY 227 CTGATATTAATCACTGCTGATGATTAACAGATTAATGCTGATGCTGATGCTGATGCA 286  
 DB 121 CTGATATTAATCACTGCTGATGATTAACAGATTAATGCTGATGCTGATGCTGATGCA 180  
 OY 287 CTGATATTAATCACTGCTGATGATTAACAGATTAATGCTGATGCTGATGCTGATGCA 346  
 DB 181 CTGATATTAATCACTGCTGATGATTAACAGATTAATGCTGATGCTGATGCTGATGCA 240  
 OY 347 GTATGCTGCTTGGCGAGGAGGCGCTTATTTACCGGAAGCTTCTGTTCAATCCACGGGT 406  
 DB 241 GTATGCTGCTTGGCGAGGAGGCGCTTATTTACCGGAAGCTTCTGTTCAATCCACGGGT 300  
 OY 407 CCTTACCGGAAGGAGGCGCTTATTTACCGGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 466  
 DB 301 CCTTACCGGAAGGAGGCGCTTATTTACCGGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
 OY 467 TAGTTTGAATTAAGTAAATTAATTTCTGATTTCTCCAAAAA 519  
 DB 361 TAGTTTGAATTAAGTAAATTAATTTCTGATTTCTCCAAAAA 413

RESULT 14

AAC00147  
 ID AAC00147 standard; cDNA; 415 BP.

XX AAC00147;  
 XX  
 XX 06-OCT-2000 (first entry)  
 DE  
 XX  
 XX

XX DE Human secreted protein 5' EST, SEQ ID NO: 145.  
 XX XX  
 KM Human: 5' EST: expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping; ss.  
 XX OS  
 OS Homo sapiens.  
 XX EP1033401-A2.  
 PN  
 XX 06-SEP-2000.  
 PD  
 XX  
 XX 21-FEB-2000; 2000EP-0200610.  
 PF  
 XX 26-FEB-1999; 99US-0122487.  
 PR  
 XX (GEST) GENSET.  
 PA  
 XX Dumas Milne Edwards J, Duclert A, Giordano J;  
 PI WPI; 2000-500381/45.  
 DR P-PSDB; AAC00141.  
 XX  
 XX Claim 1; SEQ ID 145; 71bp + CD-ROM; English.  
 PS  
 CC The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. An ORF has been identified within the  
 CC sequence. The 5' ESTs were prepared from total human RNAs or poly(A)<sup>+</sup> RNAs  
 CC derived from 30 different tissues. EST sequences usually correspond  
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are  
 CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not  
 CC well suited for isolating cDNA sequences derived from the 5' ends of  
 CC mRNAs and even in those cases where longer cDNA sequences have been  
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from  
 CC mRNAs with intact 5' ends and can therefore be used to obtain full length  
 CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,  
 CC gene therapy and chromosome mapping procedures. They are used to obtain  
 CC upstream regulatory sequences and to design expression and secretion  
 CC vectors.  
 CC  
 XX  
 XX Sequence 415 BP; 101 A; 97 C; 126 G; 91 T; 0 other;  
 SQ  
 Query Match 75.9%; Score 405.4; DB 21; Length 415;  
 Best Local Similarity 99.8%; Pred. No. 4.2e-79;  
 Matches 406; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

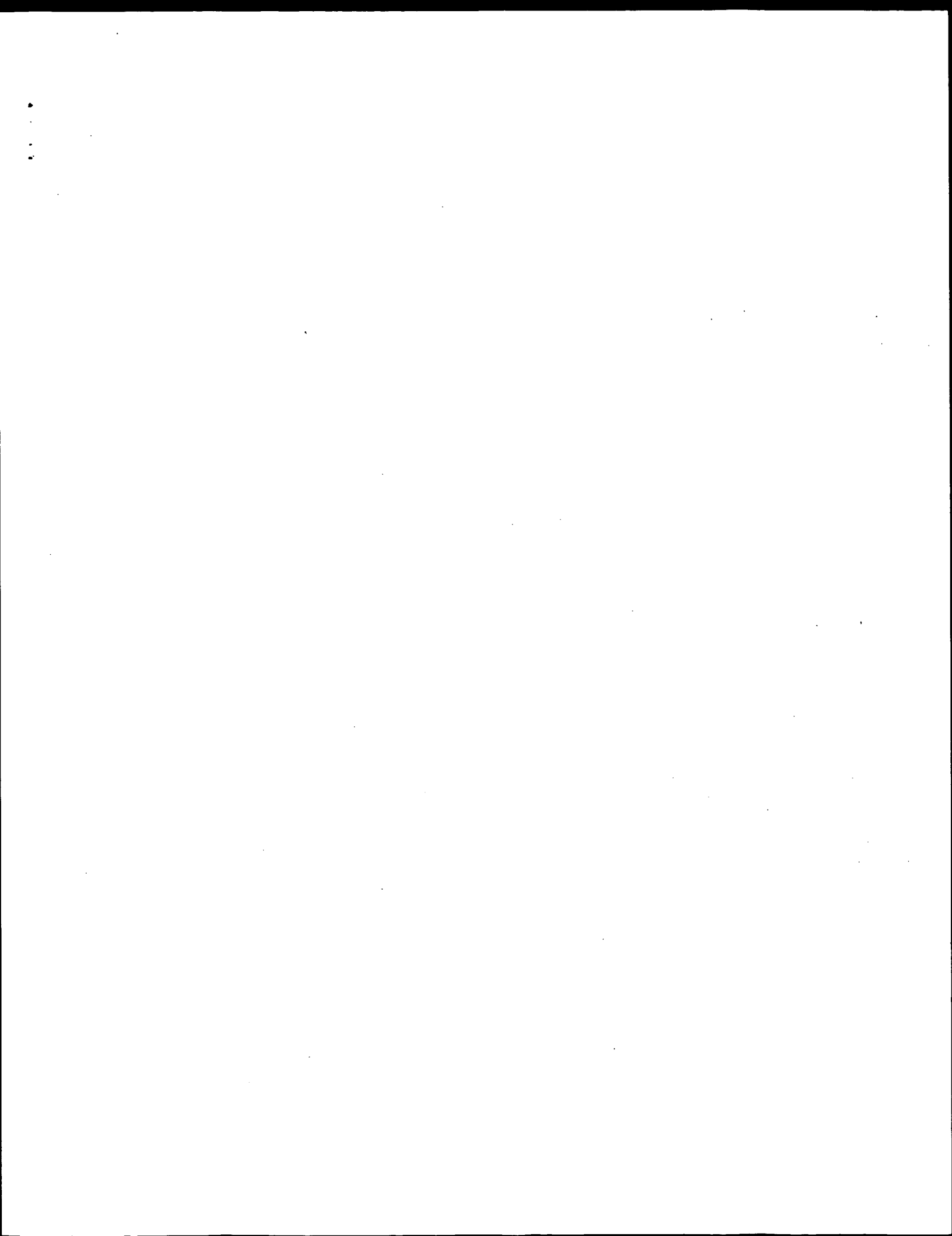
OY 375 TTACCGGAGACTCTGTTCATCCAGCGGCTCTTACGAGAAAAG 421  
 Db 369 TTACCGGAGACTCTGTTCATCCAGCGGCTCTTACGAGAAAAG 415  
 RESULT 15  
 ID AA234051 standard; cDNA; 663 BP.  
 XX AA234051;  
 AC  
 XX 07-DEC-1999 (first entry)  
 DT  
 XX Human PRO772 nucleotide sequence.  
 DE  
 XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
 KW secreted protein; transmembrane protein; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX W09946281-A2.  
 PN  
 XX 16-SEP-1999.  
 PD  
 XX 08-MAR-1999; 99WO-US05028.  
 XX  
 XX 10-MAR-1998; 98US-0077450.  
 PR 11-MAR-1998; 98US-0077632.  
 PR 11-MAR-1998; 98US-0077641.  
 PR 12-MAR-1998; 98US-0077649.  
 PR 13-MAR-1998; 98US-0077791.  
 PR 17-MAR-1998; 98US-0078004.  
 PR 20-MAR-1998; 98US-0040220.  
 PR 20-MAR-1998; 98US-0078886.  
 PR 20-MAR-1998; 98US-0078910.  
 PR 20-MAR-1998; 98US-0078936.  
 PR 25-MAR-1998; 98US-0078939.  
 PR 25-MAR-1998; 98US-0079284.  
 PR 26-MAR-1998; 98US-0079656.  
 PR 27-MAR-1998; 98US-0079663.  
 PR 27-MAR-1998; 98US-0079664.  
 PR 27-MAR-1998; 98US-0079689.  
 PR 27-MAR-1998; 98US-0079728.  
 PR 27-MAR-1998; 98US-0079786.  
 PR 30-MAR-1998; 98US-0079920.  
 PR 30-MAR-1998; 98US-0079923.  
 PR 31-MAR-1998; 98US-0080105.  
 PR 31-MAR-1998; 98US-0080107.  
 PR 31-MAR-1998; 98US-0080165.  
 PR 31-MAR-1998; 98US-0080194.  
 PR 01-APR-1998; 98US-0080327.  
 PR 01-APR-1998; 98US-0080328.  
 PR 01-APR-1998; 98US-0080333.  
 PR 01-APR-1998; 98US-0080334.  
 PR 08-APR-1998; 98US-0081049.  
 PR 08-APR-1998; 98US-0081070.  
 PR 08-APR-1998; 98US-0081071.  
 PR 09-APR-1998; 98US-0081195.  
 PR 09-APR-1998; 98US-0081203.  
 PR 09-APR-1998; 98US-0081229.  
 PR 15-APR-1998; 98US-0081817.  
 PR 15-APR-1998; 98US-0081838.  
 PR 15-APR-1998; 98US-0081893.  
 PR 15-APR-1998; 98US-0081952.  
 PR 15-APR-1998; 98US-0081955.  
 PR 21-APR-1998; 98US-0082568.  
 PR 21-APR-1998; 98US-0082569.  
 PR 22-APR-1998; 98US-0082700.  
 PR 22-APR-1998; 98US-0082704.  
 PR 22-APR-1998; 98US-0082804.  
 PR 23-APR-1998; 98US-0082767.  
 PR 23-APR-1998; 98US-0082796.

PR	27-APR-1998;	98US-0083336-	PR
PR	28-APR-1998;	98US-00833322	PR
PR	29-APR-1998;	98US-0083392.	PR
PR	29-APR-1998;	98US-0083495.	PR
PR	29-APR-1998;	98US-0083496.	PR
PR	29-APR-1998;	98US-0083499.	PR
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PR	29-APR-1998;	98US-0083545	PR
PR	29-APR-1998;	98US-0083554.	PR
PR	29-APR-1998;	98US-0083558.	PR
PR	29-APR-1998;	98US-0083559.	PR
PR	30-APR-1998;	98US-0083742.	PR
PR	05-MAY-1998;	98US-0084366-	PR
PR	06-MAY-1998;	98US-0084414.	PR
PR	06-MAY-1998;	98US-0084441.	PR
PR	07-MAY-1998;	98US-0084598.	PR
PR	07-MAY-1998;	98US-0084600.	PR
PR	07-MAY-1998;	98US-0084627.	PR
PR	07-MAY-1998;	98US-0084637.	PR
PR	07-MAY-1998;	98US-0084639.	PR
PR	07-MAY-1998;	98US-0084640.	PR
PR	07-MAY-1998;	98US-0084643.	PR
PR	13-MAY-1998;	98US-0085323.	PR
PR	13-MAY-1998;	98US-0085338.	PR
PR	13-MAY-1998;	98US-0085339.	PR
PR	15-MAY-1998;	98US-0085573.	PR
PR	15-MAY-1998;	98US-0085579.	PR
PR	15-MAY-1998;	98US-0085580.	PR
PR	15-MAY-1998;	98US-0085582.	PR
PR	15-MAY-1998;	98US-0085689.	PR
PR	15-MAY-1998;	98US-0085697.	PR
PR	15-MAY-1998;	98US-0085700.	PR
PR	15-MAY-1998;	98US-0085704.	PR
PR	18-MAY-1998;	98US-0086023.	PR
PR	22-MAY-1998;	98US-0086392.	PR
PR	22-MAY-1998;	98US-0086414.	PR
PR	22-MAY-1998;	98US-0086430.	PR
PR	22-MAY-1998;	98US-0086486.	PR
PR	28-MAY-1998;	98US-0087098.	PR
PR	28-MAY-1998;	98US-0087106.	PR
PR	28-MAY-1998;	98US-0087208.	PR
PR	30-JUL-1998;	98US-0094651.	PR
PR	11-SEP-1998;	98US-0100038.	PR
XX			
PA	(GETH ) GENENTECH INC.		
XX			
XX	Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;		
DR	WPI, 1999-551358/46.		
XX	P-PSDB; AA41713.		

Sequence	663 BP; 180 A; 137 C; 153 G; 193 T; 0 other;
Query Match	62.7%; Score 335; DB 20; Length 663;
Best Local Similarity	76.0%; Pred. No. 9.8e-64;

	Matches	504;	Conservative	0;	Mismatches	0;	Indels	159;	Gaps	1
QY	22	CGAGCTGGGGCAGAAAGT	AGGGGAGGGCGGTGCTCCGCCGGGTGGCGGTTGCTATCGCTT	81						
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QY	82	CGCAGAACCTTACTCAGGCACG	CTGAGAGAGTTGAGGGGAAATGCTGCTGGCGGGCTC	141						
Db	61	CGCAGAACCTTACTCAGGCACG	CTGAGAGAGTTGAGGGGAAATGCTGCTGGCGGGCTC	120						
QY	142	TGCAGACGCGATGATTAACGT	TGACAGCCGAAATAAATATCGCCCTCTGCTTACGTGT	201						
Db	121	TGCAGACGCGATGATTAACGT	TGACAGCCGAAATAAATATCGCCCTCTGCTTACGTGT	180						
QY	202	GAAAGGCCACGTGAAGATGCT	GGCGGTG-----	229						
Db	181	GAAAGGCCACGTGAAGATGCT	GGCGGTG-----	240						
QY	230	-----	-----	229						
Db	241	CATCGCACAGACCCCTGAACCAT	ATATTGTTATCATCTGGATTGGAAGTCACCGATTATCTT	300						
QY	230	-----	-----	229						
Db	301	ATTTTTCATACTTTTATATAT	TGACTACAGCTTGATGATTAATGGAAGTGGTATTTTGGCC	360						
QY	230	-----GATATATATCAACT	CACCTAGTGTAAACAACAGTATTCATGCTCATCGTATCTGT	282						
Db	361	TTTGCTTGAATATATATCACT	CACCTAGTGTAAACAACAGTATTCATGCTCATCGTATCTGT	420						
QY	283	GGCACTGATACCAAGAAACCA	CAACTTACAGTGTGTGAGGGGGTGTTCACATTTGTAC	342						
Db	421	GGCACTGATACCAAGAAACCA	CAACTTACAGTGTGTGAGGGGGTGTTCACATTTGTAC	480						
QY	343	AGCAGTATGCTGTCTGTGCGA	GGGGGCCCTTATTTACGGGAAGCTTCGTTCATATCCGAG	402						
Db	481	AGCAGTATGCTGTCTGTGCGA	GGGGGCCCTTATTTACGGGAAGCTTCGTTCATATCCGAG	540						
QY	403	CGGTCTCTTACCAGAAAAAGC	CTGTGCATGAAAAAAAAGAAAGTATTGTAATTTATATATAC	462						
Db	541	CGGTCTCTTACCAGAAAAAGC	CTGTGCATGAAAAAAAAGAAAGTATTGTAATTTATATATAC	600						
QY	463	TTTTTTAGTTTATATCTAAGT	ATTTAAACATTTTCTGTATCTTCCAAAAAATTTTTAAAAA	522						
Db	601	TTTTTTAGTTTATATCTAAGT	ATTTAAACATTTTCTGTATCTTCCAAAAAATTTTTAAAAA	660						
QY	523	AAA 525								
Db	661	AAA 663								

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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 10:08:11 ; Search time 65 Seconds  
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Title: US-09-801-115B-1

Perfect score: 534  
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Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	486.6	91.1	504	US-09-149-476-98	Sequence 98, Appl
2	478.6	89.6	506	US-09-149-476-252	Sequence 252, App
3	272	50.9	392	US-09-385-982-95	Sequence 95, Appl
4	50.4	9.4	1582	US-08-545-196B-10	Sequence 10, Appl
5	50.4	9.4	1582	US-08-545-196B-12	Sequence 12, Appl
6	46.8	8.8	770	US-08-865-297-5	Sequence 5, Appl
7	45.8	8.6	3761	US-08-890-865A-2	Sequence 2, Appl
8	45	8.4	961	5194596-16	Patent No. 5194596
9	45	8.4	961	5219739-16	Patent No. 5219739
10	44.6	8.4	2920	US-09-276-400-1	Sequence 1, Appl
11	44.6	8.4	2920	US-09-448-076-1	Sequence 1, Appl
12	44.6	8.4	2920	US-09-702-572-1	Sequence 1, Appl
13	44.4	8.3	333	US-08-946-026-35	Sequence 35, Appl
14	44.2	8.3	581	US-08-557-309B-22	Sequence 22, Appl
15	44.2	8.3	581	US-08-834-306-22	Sequence 22, Appl
16	44.2	8.3	581	US-08-993-674A-22	Sequence 22, Appl
17	44.2	8.3	581	US-09-256-976-22	Sequence 22, Appl
18	43	8.1	2569	US-08-569-749-1	Sequence 1, Appl
19	43	8.1	2569	PCT-US96-12860-1	Sequence 1, Appl
20	43	8.1	3238	US-08-123-934A-5	Sequence 5, Appl
21	43	8.1	3238	PCT-US94-10080-5	Sequence 5, Appl
22	42.8	8.0	1332	US-09-057-762-1	Sequence 1, Appl
23	42.8	8.0	1332	US-08-326-119A-1	Sequence 1, Appl
24	42.8	8.0	3471	PCT-US93-00227-2	Sequence 2, Appl
25	42.6	8.0	1776	US-09-149-476-59	Sequence 59, Appl
26	42	7.9	940	US-08-471-717-1	Sequence 1, Appl
27	42	7.9	2025	US-09-149-476-316	Sequence 316, App

#### ALIGNMENTS

28	42	7.9	2346	4	US-09-149-476-193	Sequence 193, App
29	41.8	7.8	742	1	US-07-847-010-12	Sequence 12, Appl
30	41.4	7.8	5852	1	US-07-867-106-2	Sequence 2, Appl
31	41.2	7.7	2671	6	5168051-9	Patent No. 5168051
32	41.2	7.7	3459	2	US-08-980-060-3	Sequence 3, Appl
33	41.2	7.7	3459	2	US-09-307-185-3	Sequence 3, Appl
34	41	7.7	218	4	US-09-480-921B-18	Sequence 18, Appl
35	40.8	7.6	1046	1	US-08-361-467B-4	Sequence 4, Appl
36	40.8	7.6	1046	1	US-08-484-332C-4	Sequence 4, Appl
37	40.6	7.6	731	1	US-08-451-405A-2	Sequence 2, Appl
38	40.6	7.6	2444	3	US-08-906-791-1	Sequence 1, Appl
39	40.6	7.6	2625	4	US-09-245-041-18	Sequence 18, Appl
40	40.4	7.6	1253	2	US-08-591-629-1	Sequence 1, Appl
41	40.4	7.6	1466	4	US-08-984-919A-10	Sequence 10, Appl
42	40.4	7.6	1466	4	US-08-984-919A-12	Sequence 12, Appl
43	40.4	7.6	1472	4	US-08-781-420-10	Sequence 10, Appl
44	40.4	7.6	1472	4	US-08-781-420-12	Sequence 12, Appl
45	40.4	7.6	1472	4	US-08-874-102-10	Sequence 10, Appl

RESULT 1  
US-09-149-476-98  
; Sequence 98, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: ROSEN ET AL.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149, 476  
; EARLIER FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040, 162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040, 333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038, 621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040, 626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040, 334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040, 336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040, 163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047, 600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047, 615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047, 597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047, 502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047, 633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047, 583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047, 617  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047, 584  
; EARLIER FILING DATE: 1997-05-23

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EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 91.1% Score 486.6; DB 4; Length 504;  
Best Local Similarity 99.0%; Pred. No. 2,7e-115;  
Matches 500; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 21 CCGAGCTGGGCGAGAGTAGGGGAGGGGCGGCTCCGCCGCGGCTGCTATTCGCT 80  
DB 1 CCGAGCTGGGCGAGAGTAGGGGAGGGGCGGCTCCGCCGCGGCTGCTATTCGCT 59  
QY 81 TCGCAGAACCTTACTAGGCGAGCCAGCTGAGAGATTGAGGGAAGTGTCTGCTGGCT 140  
DB 60 TCGCAGAACCTTACTAGGCGAGCCAGCTGAGAGATTGAGGGAAGTGTCTGCTGGCT 119  
QY 141 CTGACAGCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 200  
DB 120 CTGACAGCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 179  
QY 201 TGAAGGCGCGAGAGTAGGCTGCGGCTGATATTTATCACTGATGATCAACAGATAT 260  
DB 180 TGAAGGCGCGAGAGTAGGCTGCGGCTGATATTTATCACTGATGATCAACAGATAT 239  
QY 261 TCAATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 320  
DB 240 TCAATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 299  
QY 321 GAGGGGTGTTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 380  
DB 300 GAGGGGTGTTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 359  
QY 381 GGAAGCTTCTGTTCAATCCAGCGGCTCTTACACAGAAAAAGCCTGATGAAAAAAG 440  
DB 360 GGAAGCTTCTGTTCAATCCAGCGGCTCTTACACAGAAAAAGCCTGATGAAAAAAG 419  
QY 441 AAGTTTGTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 500  
DB 420 AAGTTTGTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 479  
QY 501 TTCTTCCAAAAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 525  
DB 480 TTCTTCCAAAAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 504

RESULT 2  
US-09-149-476-252  
Sequence 252, Application US/09149476  
Patent No. 6420526

GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163

EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,503  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,592  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,581  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,584  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,500  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,587  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,492  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,598  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,613  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,582  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,596  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,612  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,632  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,601  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,580  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,568  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,314  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,312  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,671  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,674  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,669  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,312  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,313  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,672  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056,886  
EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,889  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,630  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,878  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,662  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,872  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,882  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,637  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,903  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,888  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,879  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,880  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,894  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,636  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,874  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,588  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,585  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,586  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,590  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,594  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670

EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,882  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

## Query Match

89.6%; Score 478.6; DB 4; Length 506;

Best Local Similarity 97.4%; Pred. No. 36-113;

Matches 488; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 37 GTAGGGAGGCGGCTGCTCCGCGCGGCGGCTGCTATGCTGCGAGAACTTACCA 96  
DB 2 GCAGATTGCGCAGGACCCCGCGGCTGCTATGCTGCGAGAACTTACCA 61  
QY 97 GCGAGCAGCTGAGAGAGATTTGAGGAAAGTCTGCTGCTGCTGCGAGCGCATGGA 156  
DB 62 GCGAGCAGCTGAGAGAGATTTGAGGAAAGTCTGCTGCTGCTGCGAGCGCATGGA 121  
QY 157 TAACGTGACGCGGAAATTAACATGCGCCCTTCTGCTTCACTGTGAAGGCGACGTGA 216  
DB 122 TAACGTGACGCGGAAATTAACATGCGCCCTTCTGCTTCACTGTGAAGGCGACGTGA 181  
QY 217 GATGCTGCGGCTGATATTTATCACTGATGTAACACAGTATTCATGCTCATGATC 276  
DB 182 GATGCTGCGGCTGATATTTATCACTGATGTAACACAGTATTCATGCTCATGATC 241  
QY 277 TGTGTTGGCAGTATACCAAGCAACCAACATTTGACGTGTTGAGGGGTGTTGCACT 336  
DB 242 TGTGTTGGCAGTATACCAAGCAACCAACATTTGACGTGTTGAGGGGTGTTGCACT 301  
QY 337 TGTGACAGCATATGCTGCTTCCGACGCGGCGCTTATTTACCGGAGCTTCTGTTCA 396  
DB 302 TGTGACAGCATATGCTGCTTCCGACGCGGCGCTTATTTACCGGAGCTTCTGTTCA 361  
QY 397 TCCGACGCGCTCTTCCGAGAAAGCCGTGATGAGAAAGAAAGAGATTTGATTTTA 456  
DB 362 TCCGACGCGCTCTTCCGAGAAAGCCGTGATGAGAAAGAAAGAGATTTGATTTTA 421  
QY 457 TATTAAGTTTATGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 516  
DB 422 TATTAAGTTTATGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 481  
QY 517 AAAAAAAAAAAAAAAAAA 533  
DB 482 AAAAAAAAAAAAAAAAAA 498



```

RESULT 4
US-08-545-196B-10
; Sequence 10, Application US/08545196B
; Patent No. 6080377
;
; GENERAL INFORMATION:
; APPLICANT: MELKI, JUDITH
; APPLICANT: MUMNICH, ARNOLD
; TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
; TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
; NUMBER OF SEQUENCES: 65
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
;

```

RESULT 5  
 US-08-545-196B-12  
 Sequence 12, Application US/08545196B  
 Patent No. 6080577  
 GENERAL INFORMATION:  
 APPLICANT: MELIKI, JUDITH  
 APPLICANT: MONNICH, ARNOLD  
 TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE  
 TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY  
 NUMBER OF SEQUENCES: 65  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP  
 STREET: PO BOX 747  
 CITY: FALLS CHURCH  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22040-0747  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/545,196B  
 FILING DATE: 19-OCT-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: FARACI, C. J.  
 REGISTRATION NUMBER: 32,350  
 REFERENCE/DOCKET NUMBER: 2121-110P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 205-8000  
 TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1582 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-545-196B-12

Query Match 9.4%; Score 50.4; DB 3; Length 1582;  
Best Local Similarity 71.7%; Pred. No. 0.00078;  
Matches 66; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 443 GTTTGTAATTTATTTATTTAGTTGATAGTATTAACATATTTCTGTAAT 502  
DB 1427 GTACGCTTTTTCATCTCTATAGTTAAAGTATATATATATTTATTTT 1486  
QY 503 CTTCCAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 534  
DB 1487 TTTTAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1518

## RESULT 6

US-08-865-297-5  
Sequence 5, Application US/08865297  
Patent No. 6010853  
GENERAL INFORMATION:  
APPLICANT: Prasad V.S. Kanteti, Zhaochui Ao, and Stuart F.  
TITLE OF INVENTION: The Silva Genes, No. 6010853el Genes Involved in  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/865,297  
FILING DATE: 29-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Silverl, Jean M.  
REGISTRATION NUMBER: 39,030  
REFERENCE/DOCKET NUMBER: DPN-024  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 770 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 88..612  
US-08-865-297-5

Query Match 8.8%; Score 46.8; DB 3; Length 770;  
Best Local Similarity 61.5%; Pred. No. 0.0048;  
Matches 75; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 413 CAGAAAAAGCCTGTCATGAAAAAAGAACTTTGTATTTATTTACTTTTACTTT 472  
DB 628 CAGCACAAGATGTTACACTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 687  
QY 473 GATACAGTATTAACATATTTCTGATTTCTTCCAAAAAATTTTATTTTATTTT 532  
DB 688 CCCAGTAACAGTAATTAACCTCTTTATTTTCCAAAAAATTTTATTTTATTTT 747  
QY 533 AA 534  
DB 748 AA 749

## RESULT 7

US-08-890-865A-2  
Sequence 2, Application US/08890865A  
Patent No. 6307019  
GENERAL INFORMATION:  
APPLICANT: Constantini, Franklin  
APPLICANT: Zeng, Li  
TITLE OF INVENTION: AXIN GENE AND USES THEREOF  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: US  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,865A  
FILING DATE: 10-JUL-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/54249  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)391-0526  
TELEFAX: (212)278-0400  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3761 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-890-865A-2

Query Match 8.6%; Score 45.8; DB 4; Length 3761;  
Best Local Similarity 67.0%; Pred. No. 0.016;  
Matches 65; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 438 AAGAAGTTTGTATTTATTTATTTACTTTTGTGATAGTATTAACATATTTCT 497  
DB 3662 AATGACTTGTACATATTTCTTTCAAGCTACTTGATTAATGAATTAATTAACGTTT 3721  
QY 498 GTATCTTCCAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 534  
DB 3722 TGAACCTTCCAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 3758

## RESULT 8

US-08-890-865A-2  
Sequence 16, Application US/08890865A  
Patent No. 5194596  
APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDES, JOHN  
C.; MITCHELL, RICHARD L.

```

? SEQ ID NO 1
? LENGTH: 2920
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (143)..(2401)
US-09-276-400-1

Query Match
Best Local Similarity 68.1%; Score 44.6; DB 3; Length 2920;
Matches 62; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY      444 TTTTGTAAATTTAATTACTTTTGTAGTTGTAATACTAGATTAACAATTTTCGTATTC 503
       |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2820 TTTTACATAAATATGCTGCTAGTAAATTTTATTATTAATAAAGTGTTCTGTGATT 2879

QY      504 TTCCAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 534
       - - - - - | | | | | | | | | | | | | | | | | | | | | | | |
Db      2880 CTTCAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2910


RESULT 11
US-09-448-076-1
? Sequence 1, Application US/09448076
? Patent No. 630092
? GENERAL INFORMATION:
? APPLICANT: Khodadoust, Mehran et al.
? TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXIDASE-RELATED PROTEIN
? FILE REFERENCE: MNI-073CP
? CURRENT APPLICATION NUMBER: US/09/448,076
? EARLIER FILING DATE: 1999-11-23
? EARLIER APPLICATION NUMBER: 60/117,580
? EARLIER FILING DATE: 1999-01-27
? EARLIER APPLICATION NUMBER: 09/276,400
? EARLIER FILING DATE: 1999-03-25
? NUMBER OF SEQ ID NOS: 12
? SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1
LENGTH: 2920
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (143)..(2401)
US-09-448-076-1

Query Match
Best Local Similarity 8.4%; Score 44.6; DB 4; Length 2920;
Matches 62; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY      444 TTTTGTAAATTTAATTACTTTTGTAGTTGTAATACTAGATTAACAATTTTCGTATTC 503
       |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2820 TTTTACTATAAATGTGCTAGTAAATTTTATTATTAATAAAGTGTTCTGTGATT 2879

QY      504 TTCCAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 534
       - - - - - | | | | | | | | | | | | | | | | | | | | | | | |
Db      2880 CTTCAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2910


RESULT 12
US-09-702-572-1
? Sequence 1, Application US/09702572
? Patent No. 6391602
? GENERAL INFORMATION:
? APPLICANT: Khodadoust, Mehran
? TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND
? FILE REFERENCE: MNI-073
? CURRENT APPLICATION NUMBER: US/09/702,572
? EARLIER FILING DATE: 2000-10-31
? PRIOR APPLICATION NUMBER: 09/276,400
? PRIOR FILING DATE: 1999-03-25
```

GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skelky, Yasir A.W.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Houghton, Raymond L.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF  
NUMBER OF SEQUENCES: 65

## CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,306  
FILING DATE: 15-APR-1997

CLASSIFICATION: 424

## ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.422C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 581 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-834-306-22

## Query Match

8.3%; Score 44.2; DB 3; Length 581;

Best Local Similarity 68.5%; Pred. No. 0.02; Mismatches 28; Indels 0; Gaps 0;

Matches 61; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 446 TTGTAATTTTATTAATTAATTTAGTTGATAGTATTAACATATTTCTGATTCCT 505  
DB 484 TTTTATTAATAGTCTTTTATTAATGAGAAGATGCTGTGTTGTTGTTT 543  
QY 506 CCAAAAAAAAAAAAAAAAAAAAAA 534  
DB 544 CAAAAAAAAAAAAAAAAAAAAA 572

Search completed: June 25, 2003, 11:55:46  
Job time : 68 secs



Result No.	Score	Query Match	length	DB	ID	Description
1	534	100.0	534	10	US-09-801-115-1	Sequence 1, Appl1
2	497.2	93.1	558	9	US-10-106-696-1927	Sequence 1927, Ap
3	486.6	91.1	504	9	US-09-809-331-98	Sequence 98, Appl
4	478.6	89.6	506	9	US-09-809-331-252	Sequence 252, Appl
5	460.2	86.2	512	9	US-09-918-995-19489	Sequence 19489, A
6	425	79.6	439	9	US-09-822-846-397	Sequence 397, App
7	404	75.7	422	9	US-09-918-995-6534	Sequence 6534, App
8	335	62.7	663	9	US-09-978-295A-189	Sequence 189, App
9	335	62.7	663	9	US-09-978-697-189	Sequence 189, App
10	335	62.7	663	9	US-09-978-192A-189	Sequence 189, App
11	335	62.7	663	9	US-09-999-832A-189	Sequence 189, App
12	335	62.7	663	9	US-09-978-189-189	Sequence 189, App
13	335	62.7	663	9	US-09-978-608A-189	Sequence 189, App
14	335	62.7	663	9	US-09-978-191A-189	Sequence 189, App
15	335	62.7	663	9	US-09-978-403A-189	Sequence 189, App
16	335	62.7	663	9	US-09-978-564A-189	Sequence 189, App
17	335	62.7	663	9	US-09-978-585A-189	Sequence 189, App
18	335	62.7	663	9	US-10-017-081A-189	Sequence 189, App
19	335	62.7	663	9	US-09-978-824-189	Sequence 189, App

20	335	62.7	65.3	9	US-09-981-915A-189	Sequence 189, App
21	335	62.7	65.3	9	US-09-999-833A-189	Sequence 189, App
22	335	62.7	65.3	9	US-10-167-749-189	Sequence 189, App
23	335	62.7	65.3	9	US-09-918-585A-189	Sequence 189, App
24	335	62.7	65.3	9	US-09-978-423A-189	Sequence 189, App
25	335	62.7	65.3	9	US-10-013-921A-189	Sequence 189, App
26	335	62.7	65.3	9	US-09-978-193A-189	Sequence 189, App
27	335	62.7	65.3	9	US-10-013-929A-189	Sequence 189, App
28	335	62.7	65.3	9	US-10-016-177A-189	Sequence 189, App
29	335	62.7	65.3	9	US-09-999-830A-189	Sequence 189, App
30	335	62.7	65.3	9	US-09-978-757A-189	Sequence 189, App
31	335	62.7	65.3	9	US-09-978-187B-189	Sequence 189, App
32	335	62.7	65.3	9	US-09-978-643A-189	Sequence 189, App
33	335	62.7	65.3	9	US-10-166-709A-189	Sequence 189, App
34	305.8	57.3	63.8	9	US-09-822-846-275	Sequence 275, App
35	272	52.0	33.2	9	US-09-871-611-95	Sequence 95, App
36	224.4	42.0	45.9	10	US-09-801-115-3	Sequence 3, App
37	205	38.4	207	9	US-09-854-531-52	Sequence 52, App
38	205	38.4	207	9	US-09-854-531-229	Sequence 229, App
39	205	38.4	207	9	US-09-954-531-450	Sequence 450, App
40	205	38.4	207	10	US-09-880-107-744	Sequence 744, App
41	185.2	34.7	44.5	9	US-09-978-295A-191	Sequence 191, App
42	185.2	34.7	44.5	9	US-09-978-697-191	Sequence 191, App
43	185.2	34.7	44.5	9	US-09-978-192A-191	Sequence 191, App
44	185.2	34.7	44.5	9	US-09-999-832A-191	Sequence 191, App
45	185.2	34.7	44.5	9	US-09-978-189A-191	Sequence 191, App

RESULT 1  
US-09-801-115-1  
. Sequence 1, Application US/09801115  
. Patent No. US20020001828A1  
. GENERAL INFORMATION:  
APPLICANT: Ma, D.  
APPLICANT: Han, W.  
APPLICANT: Zhang, Y.  
APPLICANT: Song, Q.  
APPLICANT: Di, C.  
APPLICANT: Huang, J.  
APPLICANT: Tang, J.  
APPLICANT: Chen, G.  
TITLE OF INVENTION: CHEMOKINE LIKE FACTOR(CRLF) WITH CHEMOTACTIC AND HEMATOPOIETIC  
STIMULATING ACTIVITIES  
FILE REFERENCE: 10776-003-999  
CURRENT APPLICATION NUMBER: US/09/801,115  
PRIOR FILING DATE: 2001-03-07  
PRIOR APPLICATION NUMBER: PCT/CN00/00026  
PRIOR FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: 99107284.7  
PRIOR FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 8  
SEQ ID NO 1  
LENGTH: 534  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-801-115-1

Query Match 100.0%; Score 534; DB 10; Length 534;  
Best Local Similarity 100.0%; Pred. No. 1,2e+124;  
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCCCATCTGAAGTGAAAGCGGACGTGGCGGAGAATGAGGGGAGGGCGGTCTCCGCCG 60  
|||  
DB 1 GTTCCCAATCTGAAGTGAAAGCGGACGTGGCGGAGAATGAGGGGAGGGCGGTCTCCGCCG 60  
|||||  
OY CGGTGGGGGTGTATGCCTTCGCGAAGACTACTCAGGACGCCAGCTGAGAAGATTGAG 120  
|||||  
DB 61 CGGTGGGGGTGTATGCCTTCGCGAAGACTACTCAGGACGCCAGCTGAGAAGATTGAG 120  
|||||  
OY 121 GGAATGCTCTCTCTGGGCTTCGACAGCGCATGATTAACCTGCAGCCGAAATAAACA 180

Db	121	GGAAAGTGTGCTGTGGGTGTGCAGAGCGGATGATACGTGCAGGCGCAAAATTAATAAACA	180
QY	181	TGCCCCCTTCTGTTTAGTGTGAAGGCCAGGTAAATGCTGGCGGTGGATATTATCA	240
Db	181	TGCCCCCTTCTGTTTAGTGTGAAGGCCAGGTAAATGCTGGCGGTGGATATTATCA	240
QY	241	CTGACTGTGAACAAACAGTATTCATGCTATCGTATCTGTGTGGCAGCTGATACAGAAAC	300
Db	241	CTGACTGTGAACAAACAGTATTCATGCTATCGTATCTGTGTGGCAGCTGATACAGAAAC	300
QY	301	CACAAATTTGACAGTGTGTGGAGGGGTGTTTGCACTTGTACAGCAGTATGCTCTTGC	360
Db	301	CACAAATTTGACAGTGTGTGGAGGGGTGTTTGCACTTGTACAGCAGTATGCTCTTGC	360
QY	361	CGACGGGGCCCTAATTATCCGGAACCTCTGTTCAATCCGAGCGTCTTACCGAGAAAA	420
Db	361	CGACGGGGCCCTAATTATCCGGAACCTCTGTTCAATCCGAGCGTCTTACCGAGAAAA	420
QY	421	GCCTGTGCATGAAAAAAAAGAGTTTGTAAATTTATATTACTTTTAGTTGATACTAA	480
Db	421	GCCTGTGCATGAAAAAAAAGAGTTTGTAAATTTATATTACTTTTAGTTGATACTAA	480
QY	481	GTTTAAACATATTTCTGTATCTCCAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTT	534
Db	481	GTTTAAACATATTTCTGTATCTCCAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTT	534

## RESULT 2

```

US-10-106-698-1927
: Sequence 1927, Application US/10106698
: Publication No. US20030109690A1
: GENERAL INFORMATION:
:   APPLICANT: Ruben et al.
:   TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
:   FILE REFERENCE: PA005P1
:   CURRENT APPLICATION NUMBER: US/10/106,698
:   CURRENT FILING DATE: 2002-03-27
:   PRIOR APPLICATION NUMBER: PCT/US00/26524
:   PRIOR FILING DATE: 2000-09-28
:   PRIOR APPLICATION NUMBER: US 60/157,137
:   PRIOR FILING DATE: 1999-09-29
:   PRIOR APPLICATION NUMBER: US 60/163,280
:   PRIOR FILING DATE: 1999-11-03
:   NUMBER OF SEQ ID NOS: 8564
:   SOFTWARE: PatentIn Ver. 3.0
:   SEQ ID NO 1927
:   LENGTH: 558
:   TYPE: DNA
:   ORGANISM: Homo sapiens
:   FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: (514)..(514)
:   OTHER INFORMATION: n equals a,t,g, or c
:   US-10-106-698-1927

```

Query Match	93.18;	Score 497.2;	DB 9;	Length 558;
Best Local Similarity	98.48;	Pred. No. 2.2e-115;		
Matches 499; Conservative	2;	Mismatches 6;	Indels 0;	Gaps 0

QY	16	TGAAGCCGAGCTGGGCGAGAAAGTAGGGAGGGCGGTGCTCCGCCGCGGTGGCTGCTA	75
		::	
Db	11	TGAAGTCGAGAGCTGGGCGAGAAAGTAGGGAGGGCGGTGCTCCGCCGCGGTGGCTGCTA	70
QY	76	TGCCTTCGAGAGACCTACTCAGGCGAGCGAGAGTGAAGTGAAGGGAAGTGGTGGTC	135
Db	71	TGCCTTCGAGAGACCTACTCAGGCGAGCGAGTGAAGTGAAGGGAAGTGGTGGTC	130
QY	136	TGGGCTGCGAGACGGAGTGAATACGTCCAGCCGAAATAAATGATGCCCTTCCTT	195
Db	131	TGGGCTGCGAGACGGAGTGAATACGTCCAGCCGAAATAAATGATGCCCTTCCTT	190
QY	196	CAGTGTGAAGGCCACGTGAAGATGCTGGCGCTGGATATTATTCACACTACGTGTAACAC	255

Db	191	CAGGTGAAAAGGCCAGCTGAGATGCTGGGGCTGGATTTATTCACACTCCTGGTACAC	250
QY	256	AGATTTCATGCTCATCGTATCTGTGTGGACGTATACAGAAACCACAACTTGACAGT	315
Db	251	AGATTTCATGCTCATCGTATCTGTGTGGACGTATACAGAAACCACAACTTGACAGT	310
QY	316	TGGGAGAGGGGGTGTTCGCACTGTGACACACTATGCTGTGCCAGAGGGGCCCTAT	375
Db	311	TGTGTGAGGGGGTGTTCGCACTGTGACACACTATGCTGTGCCAGAGGGGCCCTAT	370
QY	376	TTACCGGAAAGCTTCTGTTCATCCACAGCGGTCCTTACAGAAAAAGCCTGTGATGAAAA	435
Db	371	TTACCGGAAAGCTTCTGTTCATCCACAGCGGTCCTTACAGAAAAAGCCTGTGATGAAAA	430
QY	436	AAAAAGAGTTTGTAAATTTTATATTAATCTTTTAGTTGATACCTAAGTATTAACATATTT	495
Db	431	AAAAAGAGTTTGTAAATTTTATATTAATCTTTTAGTTGATACCTAAGTATTAACATATTT	490
QY	496	CTGTATTCCTCCAAAAAATTTTTTTTTT	522
Db	491	CTGTATTCCTCCAAAAAATTTTTTTTTT	517

### RESULT 3

```

US-09-809-391-98
; Sequence 98, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-809-391-98

```

Query Match	91.1%;	Score 486.6;	DB 9;	Length 504;
Best Local Similarity	99.0%;	Pred. No. 9.8e-113;		
Matches 500; Conservative	0;	Mismatches 4;	Indels 1;	Gaps 1

Oy	2	CCGAGCGGGGCGGAGGTGAGGGGAGGGGGGTCGCCGGCGGGGGGGTGGCATCCGCT	80
Db	1	CCGAGCTGGGGCGAAGATGAGGGGAGGGG-ACGAGCCCGCGGGGGGTGGCATCCGCT	59
Oy	81	TCGACAGACCTACTCAGGCGCCAGCTGAGAAAGATTGAGGAAAGTGCCTCTGGGT	140
Db	60	TCGACAGACCTACTCTAGGCGCCAGCTGAGAAAGATTGAGGAAAGTGCCTCTGGGT	119
Oy	141	CTGCACAGCGAGATGATTAACGTGTGACGCCGAAAATTAATATCCGCCCTTCTGCTTCAGTG	200
Db	120	CTGCACAGCGAGATGATTAACGTGCAGCCGAAAATTAATATCCGCCCTTCTGCTTCAGTG	179
Oy	201	TGAAAGGCGACGTGAAGATGCTGCGGCTGGATATTATCACTCACTGTAACAACAGTAT	260
Db	180	TGAAAGGCCACGTGAAGATGCTGGGGTGGAATTATCACTCACTGTAACAACAGTAT	239
Oy	261	TCATGCTCATCGTATCTGTGTGGCAGCTGATACAGAAACCACAACTTGACAGTTGGTG	320
Db	240	TCATGCTCATCGTATCTGTGTGGCAGCTGATACAGAAACCACAACTTGACAGTTGGTG	299
Oy	321	GAGGGGTGTTGACACTGTGACAGCAGATCTGCTTGCCGAGAGGGGCCCTTATTAC	380
Db	300	GAGGGGTGTTGACACTGTGACAGCAGATCTGCTTGCCGAGAGGGGCCCTTATTAC	359
Oy	381	GGAAGCTTGTTCAATCCACAGCGCTCTTACCAAGAAAAGCCGTGTCATGAAAAAAAAG	440



Db 360 GGAAGCTTCTGTCATCCAGCGCTCTTACAGAAAAAGCCTGCATGAAAAAG 419  
Qy 441 AAGTTTGTATTTATTTATTTACTTTAGTTTGTACTAGTATTAACATATTTCTGTA 500  
Db 420 AAGTTTGTATTTATTTATTTACTTTAGTTTGTACTAGTATTAACATATTTCTGTA 479  
Qy 501 TTCTTCCAAAAAAGAAAAAAGAAAAA 525  
Db 480 TTCTTCCAAAAAAGAAAAAAGAAAAA 504

RESULT 4  
US-09-809-391-252  
; Sequence 252, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; CURRENT FILING DATE: 2001-03-16  
; PRIOR APPLICATION data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 252  
; LENGTH: 506  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-809-391-252

Query Match  
Best Local Similarity 89.6%; Score 478.6; DB 9; Length 506;  
Matches 484; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 37 GTAGGGAGGCGGCGTCCCGCGCGTGGCGGTTCGCTATGCTTCGAGAACTTACTCA 96  
Db 2 GCAGGATTTGGCCAGGACCCCGCGGTGGCGGTTCGCTATGCTTCGAGAACTTACTCA 61  
Qy 97 GGCAGCCAGCTGAGAAAGTTGAGGAAAGTGTGCTGCTGGTCTGCGAGAGCGATGGA 156  
Db 62 GGCAGCCAGCTGAGAAAGTTGAGGAAAGTGTGCTGCTGGTCTGCGAGAGCGATGGA 121  
Qy 157 TAACGTGACGCCGAAATTAACATGCCCTTCTGCTTCACTGTGAAAGGCCACGTGAA 216  
Db 122 TAACGTGACGCCGAAATTAACATGCCCTTCTGCTTCACTGTGAAAGGCCACGTGAA 181  
Qy 217 GATGCTGGCGCTGATTTATCACTCACTGTAACAACAGTATTCATGCTATGCTATC 276  
Db 182 GATGCTGGCGCTGATTTATCACTCACTGTAACAACAGTATTCATGCTATGCTATC 241  
Qy 277 TGTGTGGCAGCTGATACAGAAACCAACATTGACAGTGTGGAGGGGTGTTGCACT 336  
Db 242 TGTGTGGCAGCTGATACAGAAACCAACATTGACAGTGTGGAGGGGTGTTGCACT 301  
Qy 337 TGTGACAGAGTATGCTGTGCGGACGGGGCCCTTATTTACGGGAAGCTTCTGTTCAA 396  
Db 302 TGTGACAGAGTATGCTGTGCGGACGGGGCCCTTATTTACGGGAAGCTTCTGTTCAA 361  
Qy 397 TCCCGAGGGTCCCTTACCGAAGAAAGCGTGTGATGAAAGAAAGTGTGTAATTTA 456  
Db 362 TCCCGAGGGTCCCTTACCGAAGAAAGCGTGTGATGAAAGAAAGTGTGTAATTTA 421  
Qy 457 TATTAATTTTATGTTGATTAAGTATTAACATATTTCTGATTTCTTCCAAAAAAGAA 516  
Db 422 TATTAATTTTATGTTGATTAAGTATTAACATATTTCTGATTTCTTCCAAAAAAGAA 481  
Qy 517 AAAAAAAGAAAAAAGAAAAA 533  
Db 482 AAAAAAAGAAAAAAGAAAAA 498

RESULT 5  
US-09-918-995-19489

; Sequence 19489, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: FROM VARIOUS CDNA LIBRARIES  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19489  
; LENGTH: 512  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(512)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-19489

Query Match  
Best Local Similarity 86.2%; Score 460.2; DB 9; Length 512;  
Matches 462; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 57 GCGCGGTGGCGGTTGCTATCGCTTGGCAACCTTACAGGAGCGACGTGAGAGGT 116  
Db 47 GCGCGGTGGCGGTTGCTATCGCTTGGCAACCTTACAGGAGCGACGTGAGAGGT 106  
Qy 117 TGAGGGAAGTGTGCTGCTGCTGCTGCTGCAAGCGATGATTAACGTGCAAGCAATAA 176  
Db 107 TGAGGGAAGTGTGCTGCTGCTGCTGCTGCAAGCGATGATTAACGTGCAAGCAATAA 166  
Qy 177 AACATGCCCTTCTGCTTGAAGTGAAGAGCCAGCTGAAGATGCTGCGGTGATATA 236  
Db 167 AACATGCCCTTCTGCTTGAAGTGAAGAGCCAGCTGAAGATGCTGCGGTGATATA 226  
Qy 237 TCAATCACTGTGTAACAAGTATTCATGCTATGCTATGCTGTTGGCACTGATACAG 296  
Db 227 TCAATCACTGTGTAACAAGTATTCATGCTATGCTATGCTGTTGGCACTGATACAG 286  
Qy 297 AAACCAACATTTGACAGTTGTTGAGAGGGTGTGCACTTGTGACAGCAGTATGCTGC 356  
Db 287 AAACCAACATTTGACAGTTGTTGAGAGGGTGTGCACTTGTGACAGCAGTATGCTGC 346  
Qy 357 TTGCGGAGGGGGCCCTTATTTACCGAAGCTTGTGCAATCCAGGGTCTTACAGA 416  
Db 347 TTGCGGAGGGGGCCCTTATTTACCGAAGCTTGTGCAATCCAGGGTCTTACAGA 406  
Qy 417 AAAAGCTGTGATGAAGAAAAAGAAAGTGTGTAATTTTATTTACTTTTATTTGATA 476  
Db 407 AAAAGCTGTGATGAAGAAAAAGAAAGTGTGTAATTTTATTTACTTTTATTTGATA 466  
Qy 477 CTAAATTAATTAATTTCTGATTTCTTCCAAAAAAGAAAAA 522  
Db 467 CTAAATTAATTAATTTCTGATTTCTTCCAAAAAAGAAAAA 512

RESULT 6  
US-09-822-846-397  
; Sequence 397, Application US/09822846  
; Publication No. US20030027139A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: Lavallie, Edward R.  
; APPLICANT: Collins-Racie, Lisa A.  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Agostino, Michael J.

Query Match	79.68;	Score 425;	DB 9;	Length 439;
Best Local Similarity	99.88;	Pred. No. 2.8e-97;		
Matches 436;	Conservative	0;	Mismatches	0;
			Indels	1;
			Gaps	1.

RESULT 7  
US-09-918-995-6534  
; Sequence 6534, Application US/09918995  
; Publication No. US20030073623A1  
GENERAL INFORMATION

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 FROM VARIOUS CDNA LIBRARIES  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES  
 FROM VARIOUS CDNA LIBRARIES  
 FILE REFERENCE: 20411-756  
 CURRENT APPLICATION NUMBER: US/09/918,995  
 CURRENT FILING DATE: 2001-07-30

Query Match	75.7%;	Score 404;	DB 9;	Length 422;
Best Local Similarity	100.0%;	Pred. No. 5.3e-92;		
Matches 404; Conservative	0;	Mismatches	0;	Indels 0;

RESULT 8  
US-09-978-295A-189  
; Sequence 189, Application US/09978295R  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:

APPLICANT:	Baker Kevin P.
APPLICANT:	Borstlein, David
APPLICANT:	Deenoyers, Luc
APPLICANT:	Eaton, Dan
APPLICANT:	Ferrara, Napoleon
APPLICANT:	Filvaroff, Ellen
APPLICANT:	Fong, Sherman
APPLICANT:	Gao, Wei-Qiang
APPLICANT:	Gerber, Hanspeter
APPLICANT:	Gerritsen, Mary E.
APPLICANT:	Goddard, Audrey
APPLICANT:	Godowski, Paul J.
APPLICANT:	Grimaldi, J. Christophe
APPLICANT:	Gurney, Austin L.
APPLICANT:	Hillan, Kenneth J
APPLICANT:	Kjaviin, Ivar J.
APPLICANT:	Kuo, Sophia S.
APPLICANT:	Napier, Mary A.
APPLICANT:	Paai, James;
APPLICANT:	Paoni, Nicholas F.
APPLICANT:	Roy, Margaret Ann
APPLICANT:	Shelton, David L.
APPLICANT:	Stewart, Timothy A.
APPLICANT:	Tunias, Daniel

APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William T.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
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;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.7%; Score 335; DB 9; Length 663;  
Best Local Similarity 76.0%; Pred. No. 1,6e-74;

Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

QY 22 CGAGCTGGGCGAAGAGTAGGGGCGGCTCCGCGGCTGGCGGTTCTATCGCTT 81  
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QY 82 CGCAGACCTACTCAGGAGCGGAGCTGAGAGAGTTGAGGAGAAATGCTGCTGGGCTC 141  
DB 61 CGCAGACCTACTCAGGAGCGGAGCTGAGAGAGTTGAGGAGAAATGCTGCTGGGCTC 120  
QY 142 TGCAGACGCGATGATTAACGTGACCGCAAAATTAACATGCGCCCTCTCTCAGGT 201  
DB 121 TGCAGACGCGATGATTAACGTGACCGCAAAATTAACATGCGCCCTCTCTCAGGT 180  
QY 202 GAAAGCGCAGTGAAGATGCTGGGCTG----- 229  
DB 191 GAAAGCGCAGTGAAGATGCTGGGCTGCACTAATCTGACATCTATGACCTTTTAT 240  
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QY 230 ----- 229  
DB 301 ATTTTCATACCTTTATATGTAATGACTGATGATTAATGAAGTGTATTTTGGCC 360  
QY 230 -----GATATATCACTCAGTGTGTAACAAGTATTCATGCTCATGATGTGTT 282  
DB 361 TTTGCTTATATATCACTCAGTGTGTAACAAGTATTCATGCTCATGATGTGTT 420  
QY 283 GGCAGCTGATACCAAGAACCAACATTTGACAGTTGGTGGAGGGTGTGACTGTGAC 342  
DB 421 GGCAGCTGATACCAAGAACCAACATTTGACAGTTGGTGGAGGGTGTGACTGTGAC 480  
QY 343 AGCAGTATGCTGCTTGGCGAGCGGGCCCTTATTACCGAAGCTTCTGTTCAATCCAG 402  
DB 481 AGCAGTATGCTGCTTGGCGAGCGGGCCCTTATTACCGAAGCTTCTGTTCAATCCAG 540  
QY 403 CGGCTCTTACCAAGAAAGCTGTGCAATGAAAAAAGTTTGTATTTATTTATAC 462  
DB 541 CGGCTCTTACCAAGAAAGCTGTGCAATGAAAAAAGTTTGTATTTATTTATAC 600  
QY 463 TTTTACTGATCTAGTATTAACATATTTCTGATTTCTCCAAAAAATTTTAAAAA 522  
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DB 601 TTTTACTGATCTAGTATTAACATATTTCTGATTTCTCCAAAAAATTTTAAAAA 660  
QY 523 AAA 525  
DB 661 AAA 663

## RESULT 9

US-09-978-697-189  
Sequence 189, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavrin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Pan, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C27  
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CURRENT FILING DATE: 2001-10-16  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.7% Score 335 DB 9; Length 663;  
Best Local Similarity 76.0% Pred. No. 1.6e-74;  
Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

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Db 61 CGAGAACCTACTCAGGCGAGCCAGCGAGAAAGTTGAGGAAAGTGGCTGCTGGGTC 120  
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Db 121 TCGACGCGGATGATACGTGCGAGCCGAAATTAACATGCGCCCTTCTGCTGAGTGT 180  
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QY 230 ----- 229  
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Db 361 TTTGCTGATATTATCACTGCTGTAACAACATATTATTCATGCTATCTGTT 420  
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QY 343 AGCAGTATGCTGTTGCGAGAGGGGCTTATTACGGAAGCTTCTGTCATTCGAG 402  
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QY 463 TTTTATGTTATGATGATGATTAACATATTTCTGATTTCTTCCAAAAA 522  
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QY 523 AAA 525  
Db 661 AAA 663

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Sequence 189, Application US/09978192A  
Patent No. US20020177553A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
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APPLICANT: Gerber, Hanspeter  
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APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.7%; Score 335; DB 9; Length 663;  
Best Local Similarity 76.0%; Pred. No. 1.6e-74;  
Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

22 CGAGCTGGGCGAAGTAGGAGGCGGCGTCCCGCGGCGGTCTATCGCTT 81  
1 CGAGCTGGGCGAAGTAGGAGGCGGCGGTCTCCGCGGCGGTCTATCGCTT 60  
82 CGCAGACCTACTCAGCAGCCAGCTGAGAGATTGAGGAGAACTGCTGCTGCTC 141  
61 CGCAGACCTACTCAGCAGCCAGCTGAGAGATTGAGGAGAACTGCTGCTGCTC 120  
142 TGCAGACCGGATGATTAACGTGACGCCCAATAAATGCGCCCTCTGCTCAGTGT 201  
121 TGCAGACCGGATGATTAACGTGACGCCCAATAAATGCGCCCTCTGCTCAGTGT 180  
202 GAAAGCCACGTGAGATGCTGCGGCTG----- 229  
181 GAAAGCCACGTGAGATGCTGCGGCTGCACTAGTACATCTATGACCTTTTAT 240  
230 ----- 229  
241 CATCGACAAGCCCTGAGACCATATATGTTATCACTGATTTGAAGTACCGTTATCTT 300  
230 ----- 229  
301 ATTTTCATACCTTTATATGTACTCAGACTTGATGATTAATGAAGTGTATTTGGCC 360  
230 -----GATATTATCACTCACTGTAACAACAGATTCATGTCATGTCGTT 282  
361 TTTGCTGATATTAATCACTCACTGTAACAACAGATTCATGTCATGTCGTT 420  
283 GGCACATGATACCAAGAACCAACAATGACATTTGTTGAGGGGTTTGCACCTGTGAC 342  
421 GGCACATGATACCAAGAACCAACAATGACATTTGTTGAGGGGTTTGCACCTGTGAC 480  
343 AGCAGATGCTGCTGCGGAGGCGGCTTTATTAACGGAAGCTTCTGTTCAATCCAG 402  
481 AGCAGATGCTGCTGCGGAGGCGGCTTTATTAACGGAAGCTTCTGTTCAATCCAG 540  
403 CGGCTCTTACCAAGAACCTGTCATGATTAAGATTTTGTATTTATATATAC 462  
541 CGGCTCTTACCAAGAACCTGTCATGATTAAGATTTTGTATTTATATATAC 600  
463 TTTTAGTTGATACATGATTAACATATTTCTGATTTCCAAAAA 522

Db 601 TTTTAGTTGACTACTAATTAACATATTCTGATCTTCCAAAAA 660  
Qy 523 AAA 525  
Db 661 AAA 663

RESULT 11  
US-09-999-832A-189  
Sequence 189, Application US/0999832A  
Publication No. US20020192706A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Klavins, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C63  
CURRENT APPLICATION NUMBER: US/09/999, 832A  
PRIOR FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
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PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
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PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
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PRIOR FILING DATE: 1998-03-20

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PRIOR FILING DATE: 1998-03-20  
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PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336



PRIOR FILING DATE: 1998-04-27  
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PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
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PRIOR FILING DATE: 1998-05-15  
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PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.7%; Score 335; DB 9; Length 663;  
Best Local Similarity 76.0%; Pred. No. 1, 6e-74;

Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

QY 22 CGAGCTGGGCGAAGTATAGGAGGCGGCTCCGCGGAGGCGGTGCGATGCGCTT 81  
DB 1 CGAGCTGGGCGAAGTATAGGAGGCGGCTCCGCGGAGGCGGTGCGATGCGCTT 60

QY 82 CGCAGAACCTTACTAGGACCCAGCTGAGAGAGTTGAGGAGAAAGTCTGCTGGGTC 141  
DB 61 CGCAGAACCTTACTAGGACCCAGCTGAGAGAGTTGAGGAGAAAGTCTGCTGGGTC 120  
QY 142 TGCAGACGCGATGATTAAGTGCAGCCGAAATTAACATCGCCCTTCTGCTGAGTGT 201  
DB 121 TGCAGACGCGATGATTAAGTGCAGCCGAAATTAACATCGCCCTTCTGCTGAGTGT 180  
QY 202 GAAAGCGCAGTGAAGTGTGCGGCTG----- 229  
DB 181 GAAAGCGCAGTGAAGTGTGCGGCTGCGACTAGTGTGACATCTATGACCTTTTAT 240  
QY 230 ----- 229  
DB 241 CATGCGACAAAGCCCTGACCATATATTTTATCTAGTGTGAGTGCACGCTATCTT 300  
QY 230 ----- 229  
DB 301 ATTTTCATATCTTTATATGACTCAGACTGTGATGATTAATGAGTGTATTTGGCC 360  
QY 230 -----GATATTAATCACTGCTGTAACAGAGTATGCTGATCTGCTGCTGT 282  
DB 361 TTTCTTGAATTTATCACTGCTGTAACAGAGTATGCTGATCTGCTGCTGT 420  
QY 283 GGCACGTATACCAAGAACCAACATTTGAGAGGCGGCTTGCACCTGTGAC 342  
DB 421 GGCACGTATACCAAGAACCAACATTTGAGAGGCGGCTTGCACCTGTGAC 480  
QY 343 AGCAGTATGCTGCTTGCAGCGGCGCTTATTTACCAGAGCTGCTGCAATCCAG 402  
DB 481 AGCAGTATGCTGCTTGCAGCGGCGCTTATTTACCAGAGCTGCTGCAATCCAG 540  
QY 403 CGTCTCTTACAGAAAGCCTGCTGAGAAAGAGTGTGATTTATATTTATAC 462  
DB 541 CGTCTCTTACAGAAAGCCTGCTGAGAAAGAGTGTGATTTATATTTATAC 600  
QY 463 TTTTATGTTGATTAAGTATTAACATATTTCTGATTTCTTCCAAAAA 522  
DB 601 TTTTATGTTGATTAAGTATTAACATATTTCTGATTTCTTCCAAAAA 660  
QY 523 AAA 525  
DB 661 AAA 663

RESULT 12  
US-09-978-189-189  
Sequence 189, Application US/09978189  
Publication No. US20030004102A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Destroyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fond, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC7  
CURRENT APPLICATION NUMBER: US/09/978,189  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1997-11-03  
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PRIOR FILING DATE: 1998-04-01  
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PRIOR FILING DATE: 1998-04-01

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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
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PRIOR APPLICATION NUMBER: 60/085700  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.7%; Score 335; DB 9; Length 663;  
Best Local Similarity 76.0%; Pred. No. 1.6e-74;

Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

22 CGAGCTGGCGGAGAGTGGAGGCGGCTGCTCCGCGCGGTGCTGCTATGCTT 81  
1 CGAGCTGGCGGAGAGTGGAGGCGGCTGCTCCGCGCGGTGCTGCTATGCTT 60  
82 CGCAGACCTACTCAGGAGCGAGCTGAGAGAGTGGAGGAGAGTGGCTGCTGCTG 141  
61 CGCAGACCTACTCAGGAGCGAGCTGAGAGAGTGGAGAGAGTGGCTGCTGCTG 120  
142 TGCAGACGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 201  
121 TGCAGACGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180  
202 GAAAGGCCAGCGTGAAGATGCTGCGCTG----- 229  
181 GAAAGGCCAGCGTGAAGATGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCTTAT 240  
230 ----- 229  
241 CATCGCAGACGCCCTGAAACATATATTTTATCTCACTGATTTGAAGTACCGCTTATCTT 300  
230 ----- 229  
301 ATTTCATACCTTTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
230 ----- 282  
GATATTAATCACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 282  
361 TTTGCTGATATTAATCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
283 GGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 342  
421 GGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
343 AGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 402  
481 AGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
403 CGGCTGCTTACGAGAAAGCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 462  
541 CGGCTGCTTACGAGAAAGCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

OY 463 TTTTACTTGATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 522  
DB 601 TTTTACTTGATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
OY 523 AAA 525  
DB 661 AAA 663

## RESULT 13

US-09-978-608A-189  
Sequence 189, Application US/09978608A  
Publication No. US20030045462A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Williams, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C22  
CURRENT APPLICATION NUMBER: US/09/978, 608A  
CURRENT FILING DATE: 2001-10-16  
NUMBER OF SEQ ID NOS: 624  
Prior Application removed - See File Wrapper or Palm  
SEQ ID NO 189  
LENGTH: 663  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-978-608A-189

Query Match 62.7%; Score 335; DB 9; Length 663;  
Best Local Similarity 76.0%; Pred. No. 1.6e-74;

Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

22 CGAGCTGGCGGAGAGTGGAGGCGGCTGCTCCGCGCGGTGCTGCTATGCTT 81  
1 CGAGCTGGCGGAGAGTGGAGGCGGCTGCTCCGCGCGGTGCTGCTATGCTT 60  
82 CGCAGACCTACTCAGGAGCGAGCTGAGAGAGTGGAGAGAGTGGCTGCTGCTG 141  
61 CGCAGACCTACTCAGGAGCGAGCTGAGAGAGTGGAGAGAGTGGCTGCTGCTG 120  
142 TGCAGACGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 201  
121 TGCAGACGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180  
202 GAAAGGCCAGCGTGAAGATGCTGCGCTG----- 229  
181 GAAAGGCCAGCGTGAAGATGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCTTAT 240

QY	230	-----	225
Db	241	CATCGCACAAGCCCTGAAACCATATTTGTATTCACTGGATTGAATGACCGTTATCTT	300
QY	230	-----	225
Db	301	ATTTTTCATCTTTTATATGTACTGACGACTGATCGATTAATGAAGTGTTATTTGGCC	360
QY	230	-----GATATTATCACTCACTGTGTAAACAACATATTATCATGCTCATGTATCTGTGTT	285
Db	361	TTTGGCTTGATTTATATCACTCACTGTGTAAACAACATATTATTCATGCTCATGTATCTGTGTT	420
QY	283	GGCATGATATTCAGAAACCAACAATTTGACATTTGGTGGAGGGGTGTGACATTGTGAC	342
Db	421	GGACATGATATTCAGAAACCAACAATTTGACATTTGGTGGAGGGGTGTGACATTGTGAC	480
QY	343	AGCAGTATGCTGTCTTGGCCGAGGGGCCCTTATTTTACCGGAAGCTTCTGTCAATCCAG	402
Db	481	AGCAGTATGCTGTCTTGGCCGAGGGGCCCTTATTTTACCGGAAGCTTCTGTCAATCCAG	540
QY	403	CGGTCTTACCGAAGAAAGCTGTGCATGAAAAAAGAAATTTGTATTTTATTTAC	462
Db	541	CGGTCTTACCGAAGAAAGCTGTGCATGAAAAAAGAAATTTGTATTTTATTTAC	600
QY	463	TTTTAGTTGATTAAGTATTTAAACAATTTTCTGATTTCTCCAAAAAATTTTTAAAAA	522
Db	601	TTTTAGTTGATTAAGTATTTAAACAATTTTCTGATTTCTCCAAAAAATTTTTAAAAA	660
QY	523	AAA 525	
Db	661	AAA 663	

RESULT 14  
 US-09-978-191A-189  
 : Sequence 189, Application US/09978191A  
 : Publication No. US20030050239A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Ashkenazi, Avi  
 : APPLICANT: Baker Kevin P.  
 : APPLICANT: Botstein, David  
 : APPLICANT: Desnoyers, Luc  
 : APPLICANT: Eaton, Dan  
 : APPLICANT: Ferrara, Napoleon  
 : APPLICANT: Filvaroff, Ellen  
 : APPLICANT: Fond, Sherman  
 : APPLICANT: Gao, Wei-Qiang  
 : APPLICANT: Gerber, Hanspeter  
 : APPLICANT: Gerritsen, Mary E.  
 : APPLICANT: Goddard, Audrey  
 : APPLICANT: Godowski, Paul J.  
 : APPLICANT: Grimaldi, J. Christopher  
 : APPLICANT: Gurney, Austin L.  
 : APPLICANT: Hillan, Kenneth J.  
 : APPLICANT: Kijavlin, Ivar J.  
 : APPLICANT: Kuo, Sophia S.  
 : APPLICANT: Napier, Mary A.  
 : APPLICANT: Pan, James;  
 : APPLICANT: Paoni, Nicholas F.  
 : APPLICANT: Roy, Margaret Ann  
 : APPLICANT: Shelton, David L.  
 : APPLICANT: Stewart, Timothy A.  
 : APPLICANT: Tumas, Daniel  
 : APPLICANT: Williams, P. Mickey  
 : APPLICANT: Wood, William I.  
 : TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic  
 : TITLE OF INVENTION: Acids Encoding the Same  
 : FILE REFERENCE: P2630P1C4  
 : CURRENT APPLICATION NUMBER: US/09/978,191A  
 : CURRENT FILING DATE: 2001-10-15  
 : PRIOR APPLICATION NUMBER: 09/918585  
 : PRIOR FILING DATE: 2001-07-30

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7	PRIOR APPLICATION NUMBER: 60/066366
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63	PRIOR APPLICATION NUMBER: 60/081203
64	PRIOR FILING DATE: 1998-04-09
65	PRIOR APPLICATION NUMBER: 60/081229

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PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13

PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.7%; Score 335; DB 9; Length 663;  
Best Local Similarity 76.0%; Pred. No. 1.6e-74;  
Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

QY 22 CGAGCTGGCGAAGAGTGGGGGCGGCTCCCGCGGCGGCTGCTATGCT 81  
DB 1 CGAGCTGGCGAAGAGTGGGGGCGGCTCCCGCGGCGGCTGCTATGCT 60  
QY 82 CGCAGAACCTACTCAGGCGAGCCAGCTGAGAGAGTTGAGGAGAAAGTGTCTGCTGGGC 141  
DB 61 CGCAGAACCTACTCAGGCGAGCCAGCTGAGAGAGTTGAGGAGAAAGTGTCTGCTGGGC 120  
QY 142 TGCAGACGCGATGATTAAGTGAAGCGGAAATTAATCAATGCGCCCTTCTGCTCAGTGT 201  
DB 121 TGCAGACGCGATGATTAAGTGAAGCGGAAATTAATCAATGCGCCCTTCTGCTCAGTGT 180  
QY 202 GAAAGCGCAGTGAAGTGTGCGGCTG----- 229  
DB 181 GAAAGCGCAGTGAAGTGTGCGGCTGCGACTGACATGATGACCTTTTAT 240  
QY 230 ----- 229  
DB 241 CATCGACAAGCCCTGAACCATATATTGTATCACTGATTTGAAGTCAACCTATATCT 300  
QY 230 ----- 229  
DB 301 ATTTCATACCTTTATATGATGACACTGATGATTAAGTGTATTTTGGCC 360  
QY 230 -----GATTTATCACTGATGATTAAGTGTATTTTGGCC 282  
DB 361 TTGCTTGAATATTAACCTGATGATTAAGTGTATTTTGGCC 420  
QY 283 GGCACGTATACCAAGAAACCAACATGACAGTTGGGAGGGGTGTTCACTTGTGAC 342  
DB 421 GGCACGTATACCAAGAAACCAACATGACAGTTGGGAGGGGTGTTCACTTGTGAC 480  
QY 343 AGCAGTATGCTGCTTCCGAGCGGCGCTTATTTACCGAAGCTTCTGTTCAATCCAG 402  
DB 481 AGCAGTATGCTGCTTCCGAGCGGCGCTTATTTACCGAAGCTTCTGTTCAATCCAG 540  
QY 403 CGGTCTTACCAAGAAAGCTGTGATGAGAAAGAAAGTTTGAATTTATATATAC 462  
DB 541 CGGTCTTACCAAGAAAGCTGTGATGAGAAAGAAAGTTTGAATTTATATATAC 600  
QY 463 TTTTATTTGATTAAGTATTAACATATTTCTGATCTTCCAAAAAATTTTATTTTAT 522  
DB 601 TTTTATTTGATTAAGTATTAACATATTTCTGATCTTCCAAAAAATTTTATTTTAT 660  
QY 523 AAA 525  
DB 661 AAA 663

RESULT 15  
US-09-978-403A-189

Sequence 189, Application US/09978403A  
Publication No. US20030050240A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Flvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James:  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C17  
CURRENT APPLICATION NUMBER: US/09/978,403A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
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 PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.7%; Score 335; DB 9; Length 663;  
 Best Local Similarity 76.0%; Pred. No. 1.6e-74;

Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

QY 22 CGAGCTGGGCGAGAGTAGGGGAGGGGCTGCTCCCGCGGCTGGCGGTTGCTATGCTT 81  
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 DB 61 CGAGAACCTACTCAGGACCCAGCTGAGAGAGTTGAGGGAAGTGTGCTGCTGGGTC 120  
 |||||||  
 QY 142 TGCAGACGCGATGATTAACGTGACGCCGAAATTAACATGCGCCCTTCTGCTCACTGT 201  
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 DB 121 TGCAGACGCGATGATTAACGTGACGCCGAAATTAACATGCGCCCTTCTGCTCACTGT 180  
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 QY 202 GAAAGGCCACGTGAAGTGTGCGGCTG----- 229  
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DB 181 GAAAGGCCACGTGAAGTGTGCGGCTGCGACTACTGTGACATCTATGACTTTTAT 240  
 QY 230 ----- 229  
 DB 241 CATGCAAGCCCGCTGAACCATATATGTTATCATCTGATTTGAAGTCAACGTTATCTT 300  
 QY 230 ----- 229  
 DB 301 ATTTTCATCTTTATATGACTGACACTGATGATATATGAAGTGTATTTTGGCC 360  
 QY 230 -----GATTTTCAACTCTGTTACACAGTATTTATGCTCATGCTATCTGT 282  
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 DB 361 TTGCTGATATATTAACCTACCTGTAACACAGTATTCATGCTCATCTATCTGT 420  
 QY 283 GGCACCTGATACCAAAACCAATGACAGTGGGAGGGGTTGCTGCTGAC 342  
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 DB 421 GGCACCTGATACCAAAACCAATGACAGTGGGAGGGGTTGCTGCTGAC 480  
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 QY 343 AGCAGTATGCTGTCTGCGGAGGGGCTTATTTACCGAAGCTTCTGTTCAATCCAG 402  
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 DB 481 AGCAGTATGCTGTCTGCGGAGGGGCTTATTTACCGAAGCTTCTGTTCAATCCAG 540  
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 DB 541 CGGTCTTACCAAAAAAGCTGTGATGAAAAAAGTTTGTATTTATTTATAC 600  
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 QY 463 TTTTATGTTAGTACTAGTATTAACATATTTCTGTTTCCAAAAA 522  
 |||||||  
 DB 601 TTTTATGTTAGTACTAGTATTAACATATTTCTGTTTCCAAAAA 660  
 |||||||

Search completed: June 25, 2003, 12:47:19  
 Job time: 143 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 07:52:21 ; Search time 1418 Seconds  
(without alignments)  
6099.006 Million cell updates/sec

Title: US-09-801-115b-1

Perfect score: 534  
Sequence: 1 gtcccaatctgaagtgaag.....aaaaaaaaaaaaaaaaaaaaa 534

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

EST: \*  
1: em\_estbda: \*  
2: em\_estbhm: \*  
3: em\_estln: \*  
4: em\_estnu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_hlc: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_hlc: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: gb\_gss: \*  
18: em\_gss\_hum: \*  
19: em\_gss\_inv: \*  
20: em\_gss\_pln: \*  
21: em\_gss\_vrt: \*  
22: em\_gss\_fun: \*  
23: em\_gss\_man: \*  
24: em\_gss\_mus: \*  
25: em\_gss\_other: \*  
26: em\_gss\_pro: \*  
27: em\_gss\_rtd: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	505.8	94.7	524	12	BG705303
2	492.4	92.2	510	12	BG249994
3	491.8	92.1	510	12	BF399486
4	487	91.2	781	13	BG529072
5	485.4	90.9	487	13	BM472086
6	482.4	90.3	534	12	BG031757

7	468.2	87.7	529	12	BF691818
8	468	87.6	468	12	BE109912
9	467.6	87.6	930	12	BF203359
10	452	84.6	452	9	AT078580
11	445	83.3	453	9	AT743235
12	432.4	81.0	533	10	AV754613
13	430.4	80.6	432	9	AA429945
14	427	80.0	427	9	AA455042
15	422	79.0	423	9	AI128804
16	415.2	77.8	443	12	BG613984
17	413.8	77.5	432	10	AV759888
18	412.4	77.2	543	12	BG532587
19	403	75.5	815	12	BF215121
20	402.6	75.4	409	9	AI826623
21	400.4	75.0	404	13	BM553628
22	399.4	74.8	402	9	AI989747
23	399	74.7	399	9	AA516431
24	394.4	73.9	396	10	AM183193
25	391	73.2	391	9	AI989739
26	386	72.3	386	9	AA911088
27	384.4	72.0	386	9	AA989129
28	381	71.3	395	9	AI141284
29	374.4	70.1	468	14	W52820
30	363	68.0	522	14	W38899
31	361.6	67.7	389	9	AA305052
32	357.6	67.0	456	12	BE875161
33	353	66.1	353	9	AI265924
34	349.4	65.4	692	11	AF151058
35	337.6	63.2	409	14	N89912
36	337.2	63.1	380	9	AA477156
37	331.4	62.1	333	9	AA987264
38	331.4	62.1	583	14	BC013860
39	329.8	61.8	789	12	BE737159
40	327.6	61.3	381	9	AA644621
41	326.2	61.1	326	12	BF388158
42	324.4	60.7	326	9	AI263361
43	324	60.7	325	9	AI371387
44	319.4	59.8	678	13	BI561562
45	319	59.7	319	9	AI349474

## ALIGNMENTS

RESULT 1  
LOCUS BG705303 524 bp mRNA linear EST 07-MAY-2001  
DEFINITION 602687808F1 NIH\_MGC\_95 Homo sapiens CDNA clone IMAGE:4820568 5',  
mRNA sequence.

ACCESSION BG705303  
VERSION BG705303.1 GI:13979504  
KEYWORDS EST.

## SOURCE

human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 524)

NH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT Robert Strausberg, Ph.D.

Email: [cgap@remail.nih.gov](mailto:cgap@remail.nih.gov)

Tissue Procurement: Miklos Palokovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shihai

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM10725 row: 0 column: 01

High quality sequence stop: 521.

Location/Qualifiers

FEATURES

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source
1. 524
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4820568"
/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
/Note="Organ: brain; Vector: Bluescript (modified
Bluescript KS+); Site:1: BamHI; Site:2: SalI; xhoI (gtcgag
); Oligo-dr primed using primer 5'-TTTCTTTTCTTTTCTTTT-3',
size-selected for average insert size 2.5 kb and
normalized to 10^5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGR, National
Institutes of Health). Note: this is a NIH_MGC library."

BASE COUNT      142 a      113 c      138 g      131 t
ORIGIN

Query Match      94.7%; Score 505.8; DB 12; Length 524;
Best Local Similarity 99.6%; Pred. No. 8.3e-66;
Matches 507; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 GTGAAGCCGAGCTGGGAGAGAGGGGCGGTCTCCGCCGCGGTGGCGTGTCT 74
DB 4 GGGAGGCCGAGCTGGGAGAGAGGGGCGGTCTCCGCCGCGGTGGCGTGTCT 63
QY 75 ATCGCTTCGAGAACTACTACTAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 134
DB 64 ATCGCTTCGAGAACTACTACTAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
QY 135 CTGGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
DB 124 CTGGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 183
QY 195 TCAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254
DB 184 TCAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
QY 255 CAGTATTCATGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 314
DB 244 CAGTATTCATGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303
QY 315 TTGGTGGAGGGGCTTGGCACTGTGACAGACATGATGCTGCTGCTGCTGCT 374
DB 304 TTGGTGGAGGGGCTTGGCACTGTGACAGACATGATGCTGCTGCTGCTGCT 363
QY 375 TTACCGGAGAGCTTCTGTCATCCAGCGGCTTACCGAGAGAGAGAGAGAG 434
DB 364 TTACCGGAGAGCTTCTGTCATCCAGCGGCTTACCGAGAGAGAGAGAGAG 423
QY 435 AAAAAGAGTTTGTATTTTATTTATTTATTTATTTATTTATTTATTTATTT 494
DB 424 AAAAAGAGTTTGTATTTTATTTATTTATTTATTTATTTATTTATTTATTT 483
QY 495 TCTGTATTTCTTCAAAAAAATTTTATTTTATTTTATTTTATTTTATTTT 523
DB 484 TCTGTATTTCTTCAAAAAAATTTTATTTTATTTTATTTTATTTTATTTT 512

RESULT 2
LOCUS      BG249994      962 bp      mRNA      linear      EST 13-FEB-2001
DEFINITION 602362062F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4470662 5',
ACCESSION  BG249994
VERSION     BG249994.1 GI:12759810
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 962)

```

```

AUTHORS      NIH-MGC http://mgc.ncl.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-remail.nih.gov
              Tissue Procurement: ATCC
              CDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: The I.M.A.G.E. Consortium (ILNI)
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/ILNI at:
              http://image.llnl.gov
              Plate: LLM10288 row: k column: 15
              High quality sequence stop: 516.
              Location/Qualifiers
              1. 962
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="IMAGE:4470662"
              /clone_lib="NIH_MGC_90"
              /tissue_type="adenoecarcinoma, cell line"
              /lab_host="DH10B (phage-resistant)"
              /note="Organ: liver; Vector: pCMV-Sport6; Site:1: NotI;
              Site:2: SalI; Cloned unidirectionally; oligo-dr primed.
              Average insert size 1.7 kb. Library enriched for
              full-length clones and constructed by Life Technologies.
              Note: this is a NIH_MGC library."

BASE COUNT      334 a      199 c      288 g      141 t
ORIGIN

Query Match      92.2%; Score 492.4; DB 12; Length 962;
Best Local Similarity 99.6%; Pred. No. 5e-64;
Matches 504; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 29 GCGAGAGATGAGGAGAGGCGGTCTCCGCCGCGGTGGCTATCGCTTGCAGAA 88
DB 1 GCGAGAGATGAGGAGAGGCGGTCTCCGCCGCGGTGGCTATCGCTTGCAGAA 60
QY 89 CCTACTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 148
DB 61 CCTACTCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 149 GCGATGATTAACGTGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 208
DB 121 GCGATGATTAACGTGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 209 CACGTGAAGATGCTGCGGCTGATTTATCAATCATCTGTAACAACAGTATCATGCTC 268
DB 181 CACGTGAAGATGCTGCGGCTGATTTATCAATCATCTGTAACAACAGTATCATGCTC 240
QY 269 ATCGTATCTGTTGGCACTGATATACAGAGAGAGAGAGAGAGAGAGAGAGAG 328
DB 241 ATCGTATCTGTTGGCACTGATATACAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 329 TTTCACCTTGTGACAGCATATGCTGCTTCCGAGAGGGGCTTATTTACCGGAGCTT 388
DB 301 TTTCACCTTGTGACAGCATATGCTGCTTCCGAGAGGGGCTTATTTACCGGAGCTT 360
QY 389 CTGTCATATCCAGAGGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 448
DB 361 CTGTCATATCCAGAGGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
QY 449 TAATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 508
DB 420 TAATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 479
QY 509 AAAAAAAAAAAAAAAAAAAAAA 534
DB 480 CAAAAAAAAAAAAAAAAAAAAA 505

RESULT 3
REFERENCE  1 (bases 1 to 962)

```

	Query Match	Similarity	92.1%	Score	491.8	DB	12	Length	510
	Best Local	Similarity	99.6%	Pred. No.	9.9e-64				
	Matches	493	Conservative	0	Mismatches	2	Indels	0	Gaps
QY	28	GGGCGAGAAGTAGGGGAGGGCGGTCCTCCGCCGGTGGCGGTTCTATCGCTTGCAGA	87						
	493								
DB	495	GGGCGAGAAGTAGGGGAGGGCGGTCCTCCGCCGGTGGCGGTTCTATCGCTTGCAGA	436						
QY	88	ACCTCTCAGGACGACCTGACGAGACTTTAGGGGAAAGTGCTGTGCTGGGTCTGCAGCA	147						
	435								
DB	435	ACCTCTCAGGACGACCTGACGAGAGTGTGGGAAAGTGCTGTGCTGGGTCTGCAGCA	376						
QY	148	CGCGATGATTAACCTGTCAGCCGAAAATTAACATCGCCCTTCTCTCAGTGTGAAAG	207						
	375								
DB	375	CGCGATGATTAACCTGTCAGCCGAAAATTAACATCGCCCTTCTCTCAGTGTGAAAG	316						
QY	208	CCACGTGAAGATGCTGCGGCTGGATATTATCAACTCAGTGGTAAACAAGTATTATGCT	267						
	315								
DB	315	CCACGTGAAGATGCTGCGGCTGGATATTATCAACTCAGTGGTAAACAAGTATTATGCT	256						

Query Match	Score 487;	DB 12;	Length 781;
Best Local Similarity	98.7%;	Pred. NO. 3, 7e-63;	





	Y	D	RESULT 8 BF109912/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES source
	502 TCTTCAAAAAA 514               482 TCTTGCGAGACA 494		
	BF109912 7171f03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3526805 3' similar to TR:Q9U4I Q9U4I CHEMOKINE-LIKE FACTOR 1. [1] ; mRNA sequence. BF109912 BF109912.1 GI:10939602 EST.	468 bp mRNA linear EST 20-OCT-2000	
	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: scgaps-remail.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -400P from Glibco. Location/Qualifiers 1..468 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_IMAGE=3526805" /clone_id="Soares.NSF_F8_9W_OT_PA_P_S1" /lab_host="DH10B" /note="Organ: pooled; Vector: pTY3D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clones: Soares NbHSF pool 1: 309384-310919, 333208-325885 Soares NbZNF pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NbZNF8-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322823, 326280-326653 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Benicio Soares and M. Fatima Bonalao."		
	BASE COUNT 127 a 116 c 102 g 123 t ORIGIN		
	Query Match 87.6%; Score 468; DB 12; Length 468; Best Local Similarity 100.0%; Pred. NO. 3.4e-60; Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
	46 GGCGGTCTCCGCCGCGGGTGGCTGTATCAGCTTCGCAGAACCTACTACGAGCCAG 105       468 GGGGTGTCTCCGCCGCGGGTGGCTGTATCAGCTTCGCAGAACCTACTACGAGCCAG 409       106 CTGAAGAAGTTGAGGAGAAAGTCTGCTGTGGGTCTGACAGCGCATGATGAACGTGCA 165       408 CTGAAGAAGTTGAGGAGAAAGTCTGCTGTGGGTCTGACAGCGCATGATGAACGTGCA 349       166 GCCAAAATAAACAANTGGCCCCCTCTGCTTACGTGAAGGCCACGTAAGATGCTGCG 225       348 GCCAAAATAAACAANTGGCCCCCTCTGCTTACGTGAAGGCCACGTAAGATGCTGCG 289       226 GCTGATATTATTCACATCTGATGAACAAGATATTCATGCTCAATGATGTTGGGC 285       288 GCTGATATTATTCACATCTGATGAACAAGATATTCATGCTCAATGATGTTGGGC 229		

OY	286	ACGATATCCGAGAAACCAACATTTGACAGTGGTGGAGGGGTGTTGGACTTGGACAGC	345
Db	228	ACTGATACCAAAACACACACATTGACGTTGGTGGAGGGGTGTTGGACTTGGACAGC	169
OY	346	AGATAGCTGTCTTCCGCGAGGGGGCCCTATTATTACCGGAAGCTTGTTCATCCACGG	405
Db	168	AGTATGCTGTCTTCCGCGAGGGGGCCCTATTATTACCGGAAGCTTGTTCATCCACGG	109
OY	406	TCCTTACCAAAAAAGCGTGGCATGAAAAAAGAAAGTTTGTATTTTATTTACTTT	465
Db	108	TCCTTACCAAAAAAGCGTGGCATGAAAAAAGAAAGTTTGTATTTTATTTACTTT	49
OY	466	TTAGTTGATCTAGTATTAACATATTTCTGATCTTCCAAAAA	513
Db	48	TTAGTTGATCTAGTATTAACATATTTCTGATCTTCCAAAAA	1
RESULT 9			
BF203359		930 bp	mRNA
LOCUS			linear
DEFINITION			EST 06-NOV-2000
ACCESSION	BF203359		
VERSION	BF203359.1		
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
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1..930			
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/db_xref="taxon:9606"			
/clone="IMAGE:4098496"			
/clone_lib="NIH_MGC_17"			
/tissue_type="rhabdomyosarcoma"			
/lab_host="DH10B (phage-resistant)"			
/note="Organ: muscle; Vector: pORF7; Site.1: EcoRI; Site.2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity	87.6%;	Score 467.6;	DB 12; Length 930;
Matches	503; Conservative	0; Mismatches	4; Indels
			3; Gaps
			3;
OY	25	GCTGGGCGAGAGTAGGGGAGGGCGGTCTCCCGCGGTGGCGTTGATCGCTTCCG	84
Db	1	GCTGGGCGAGAGTAGGGGAGGGCGGTCTCCCGCGGTGGCGTTGATCGCTTCCG	60
OY	85	AGAACCTACTAGCAGCAGCTGTAGAAAGTTTAGGAAAGTCTGCTGTGGGTCTGC	144



Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was from PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneids: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares NB2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NB2HR-9w pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 123 a 109 c 93 g 128 t  
ORIGIN

## Query Match

Best Local Similarity 98.9%; Score 445; DB 9; Length 453;  
Pred. No. 8.7e-57;

Matches 448; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

OY 61 CGGTGCGGTGCTATCGCTCGCAGAACCTACTAGGAGCGCAGCTGAGAGTTGAG 120
    |||||
DB 453 CGGTGCGGTGCTATCGCTCGCAGAACCTACTAGGAGCGCAGCTGAGAGTTGAG 394
OY 121 GGAAGTGTGCTGTGCTGCTGCGACAGCGATGATTAAGTGCAGCCGAAATTAACA 180
    |||||
DB 393 GGAAGTGTGCTGTGCTGCTGCGACAGCGATGATTAAGTGCAGCCGAAATTAACA 334
OY 181 TGGCCCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
    |||||
DB 333 TGGCCCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 274
OY 241 CTCACGTGTACAGACAGTATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
    |||||
DB 273 CTCACGTGTACAGACAGTATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 214
OY 301 CACACATTTGACAGTGTGAGAGGGGTGTTGACACTGTGACAGAGATGCTGCTGCTGCTG 360
    |||||
DB 213 CACACATTTGACAGTGTGAGAGGGGTGTTGACACTGTGACAGAGATGCTGCTGCTGCTG 154
OY 361 CGACGGGGGCTTATTTACCGAAGCTTCTGTCATGCCAGCGCTCTTACCAAAAAA 420
    |||||
DB 153 CGACGGGGGCTTATTTACCGAAGCTTCTGTCATGCCAGCGCTCTTACCAAAAAA 94
OY 421 GCGTGTGATGAAAAAAGAGTTTGTATTTATATTAATTTAGTTTATGATATCA 480
    |||||
DB 93 GCGTGTGATGAAAAAAGAGTTTGTATTTATTAATTTAGTTTATGATATCA 34
OY 481 GTATTAACATATTTCTGTATTTCTTCCAAAAA 513
    |||||
DB 33 GTATTAACATATTTCTGTATTTAAAAA 1

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RESULT 12  
AV754613 533 bp mRNA linear EST 19-OCT-2000  
AV754613 TP Homo sapiens cDNA clone TPAOAI1 5', mRNA sequence.

DEFINITION  
AV754613  
VERSION  
AV754613.1 GI:10912461  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens

REFERENCE  
Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS  
Song, H., Peng, Y., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N.,  
Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu  
W., Tu, Y., Jia, D., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Ye, M.,  
Zhang, Q., Han, Z., Chen, Z., and Chen, J.  
TITLE  
Homo sapiens TP library cDNA clones  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Qinghua Zhang

Shanghai Institute of Endocrinology, Rui-Jin Hospital  
197 Rui-Jin II Road, Shanghai 200025, P. R. China  
Tel: 86-21-64370045(ex. 663333)  
Fax: 86-21-64743206  
Email: mshisms.stn.sh.cn  
This clone is available at Shanghai Hematology Institute in  
Shanghai.  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.  
Location/Qualifiers  
1. .533  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="TPAOAI1"  
/clone\_lib="tp"  
/tissue\_type="pituitary tumor"  
/dev\_stage="adult"  
/lab\_host="BM25.8"  
/note="Vector: pTR1pEx2; Site\_1: sflia; Site\_2: sflib"

## FEATURES

SOURCE

BASE COUNT 149 a 112 c 145 g 120 t  
ORIGIN

## Query Match

Best Local Similarity 95.5%; Score 432.4; DB 10; Length 533;  
Pred. No. 5.6e-35;

Matches 487; Conservative 0; Mismatches 12; Indels 11; Gaps 4;

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OY 13 AAGTGAAGCCAGCTGCGGAGAGTAGGGAGGCGGCTCGCCGCGGCGGCTTG 72
    |||||
DB 35 AGGGGAAGCCAGCTGCGGAGAGTAGGGAGGAGGCGGCTCGCCGCGGCTTG 91
OY 73 CTATGCTTGCAGAACCTACTGAGCAGCCAGCTGAGAGAGTGTGAGGAAAGTCTGC 132
    |||||
DB 92 CTATGCTTGCAGAACCTACTGAGCAGCCAGCTGAGAGAGTGTGAGGAAAGTCTGC 151
OY 133 TGCAGGCTGCGACAGCGAGTATGATAGCGAGCGAGCGAATTAACATCGCCCTTTC 192
    |||||
DB 152 TGCAGGCTGCGACAGCGAGTATGATAGCGAGCGAGCGAATTAACATCGCCCTTTC 210
OY 193 CTTGAGTGTGAAGGCCAGCTGAGAGATGCTGCGGCTGATATTCACATCTGTAAC 252
    |||||
DB 211 CTTGAGTGTGAAGGCCAGCTGAGAGATGCTGCGGCTGATATTCACATCTGTAAC 270
OY 253 AACAGATTCATGCTCATGCTGATGCTGTTGGACATGATACAGAAACCAACATTTGAC 312
    |||||
DB 271 AACAGATTCATGCTCATGCTGATGCTGTTGGACATGATACAGAAACCAACATTTGAC 330
OY 313 AGTTGGGAGAGGGGTGTTGCACTTGTGACAGAGATGCTGCTGCTGCGAGGGGCGCT 372
    |||||
DB 331 AGTTGGGAGAGGGGTGTTGCACTTGTGACAGAGATGCTGCTGCTGCGAGGGGCGCT 387
OY 373 TATTTACCGGAAGCTTGTGTCATCCAGCGGCTCTTACAGAAAAAGCCTGTGATGA 432
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DB 388 TATTTACCGGAAGCTTGTGTCATCCAGCGGCTCTTACAGAAAAAGCCTGTGATGA 447
OY 433 AAAAAAAGAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 492
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DB 448 AAAAAAAGAG---GTAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 503
OY 493 TTTCTGATTTCTTCCAAAAA 522
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DB 504 TTTCTGATTTCTTCCAAAAA 533
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## RESULT 13

AA429945/c 432 bp mRNA linear EST 16-OCT-1997  
AA429945

DEFINITION  
AA429945  
VERSION  
AA429945  
KEYWORDS  
EST.  
SOURCE  
human.

ORGANISM  
Homo sapiens



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 432)

REFERENCE  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R., and Wilson, R.

TITLE  
WashU-Merck EST Project 1997

JOURNAL  
Unpublished (1997)

COMMENT  
Contact: Wilson RK  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estevatson.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -41m13 fwd. ET from Amersham  
High quality sequence stop: 421.

FEATURES  
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/clone="IMAGE:781291"  
/clone\_lib="Soares\_testis\_NHT"  
/sex="male"  
/lab\_host="DH10B"  
/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5' TGTTACCATCTGAGTGGAGGCGCCCAATTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT  
119 a 101 c 92 g 120 t

Query Match 80.6%; Score 430.4; DB 9; Length 432;  
Best Local Similarity 99.8%; Pred. No. 1.3e-54;  
Matches 431; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

81 TCGGAGAACCTACTCAGGAGCCAGCTGAGAGATGGGAGAAAGTGTGCTGGGT 140  
432 TCGGAGAACCTACTCAGGAGCCAGCTGAGAGATGGGAGAAAGTGTGCTGGGT 373  
141 CTGAGAGCGAGTGAATGATGTCAGCCGAAATTAACATGCCCTTCTGCTCAGTG 200  
372 CTGAGAGCGAGTGAATGATGTCAGCCGAAATTAACATGCCCTTCTGCTCAGTG 313  
201 TGAAGGCGAGTGAATGATGTCAGCCGAGTGAATTAACATGCCCTTCTGCTCAGTG 260  
312 TGAAGGCGAGTGAATGATGTCAGCCGAGTGAATTAACATGCCCTTCTGCTCAGTG 253  
261 TCATGCTCATCTGATCTGTTGGCAGTATACCAAGAAACCAACATTTGAGTTGGT 320  
252 TCATGCTCATCTGATCTGTTGGCAGTATACCAAGAAACCAACATTTGAGTTGGT 193  
321 GAGGGGTGTTGCACTTGTGACAGCAGTATGCTGTGCTGCGAGCGGGCCCTTATTTAC 380  
192 GAGGGGTGTTGCACTTGTGACAGCAGTATGCTGTGCTGCGAGCGGGCCCTTATTTAC 133  
381 GGAAGTCTGTTCAATCCAGCGGCTTACACAGAAAAGCCTGTGCTGAAAAAAG 440  
132 GGAAGTCTGTTCAATCCAGCGGCTTACACAGAAAAGCCTGTGCTGAAAAAAG 73  
441 AAGTTTGAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 500  
72 AAGTTTGAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 13  
501 TTTCTTCACAAA 512

||||| |||  
12 TTTCTTCACAAA 1

Db 12 TTTCTTCACAAA 1

RESULT 14  
AA455042/c  
LOCUS  
DEFINITION  
AA455042 427 bp mRNA linear EST 06-JUN-1997  
aa04a07.s1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:812244  
3', mRNA sequence.

ACCESSION  
AA455042  
VERSION  
AA455042.1 GI:2177818  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (bases 1 to 427)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R., and Wilson, R.

TITLE  
WashU-Merck EST Project 1997

JOURNAL  
Unpublished (1997)

COMMENT  
Contact: Wilson RK  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estevatson.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -41m13 fwd. ET from Amersham  
High quality sequence stop: 395.

FEATURES  
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1. 427  
/organism="Homo sapiens"  
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/clone="IMAGE:812244"  
/clone\_lib="Soares\_NhHMPu\_S1"  
/tissue\_type="Pooled human melanocyte, fetal heart, and pregnant uterus"  
/lab\_host="DH10B"  
/note="Organ: mixed (see below); Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBM, pregnant uterus NBHPU, and fetal heart NBH19M) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT  
119 a 101 c 91 g 116 t

Query Match 80.0%; Score 427; DB 9; Length 427;  
Best Local Similarity 100.0%; Pred. No. 4.1e-54;  
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

81 TCGGAGAACCTACTCAGGAGCCAGCTGAGAGATGGGAGAAAGTGTGCTGGGT 140  
427 TCGGAGAACCTACTCAGGAGCCAGCTGAGAGATGGGAGAAAGTGTGCTGGGT 368  
141 CTGAGAGCGAGTGAATGATGTCAGCCGAAATTAACATGCCCTTCTGCTCAGTG 200  
367 CTGAGAGCGAGTGAATGATGTCAGCCGAAATTAACATGCCCTTCTGCTCAGTG 308  
201 TGAAGGCGAGTGAATGATGTCAGCCGAGTGAATTAACATGCCCTTCTGCTCAGTG 260  
307 TGAAGGCGAGTGAATGATGTCAGCCGAGTGAATTAACATGCCCTTCTGCTCAGTG 248



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 25, 2003, 11:55:49 ; Search time 1313 Seconds  
(without alignments)  
2194.347 Million cell updates/sec

Title: US-09-801-115B-2

Perfect score: 508  
Sequence: 1 MDNVQPKIKHRPFCESVKGH.....LNPDSGPYQKKPVEKKEVL 99

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q/cgcn2.1/USPFO.spool/US09801115/runat\_20062003\_141102\_13583/app.query.fasta\_1.263  
-DB=genembl -QFWT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
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-DOCAALIGN=200 -THR.SCORE=DCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFWT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
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2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*

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30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rtd:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	100.0	515	6	AX061624 Sequence
2	508	100.0	530	9	AF096895 Homo sapi
3	471.5	92.8	655	9	AF057306 Homo sapi
4	471.5	92.8	669	6	AX061665 Sequence
5	471.5	92.8	688	9	BC004380 Homo sapi
6	471.5	92.8	689	9	AF135380 Homo sapi
7	366	72.0	485	11	G30204
8	339.5	66.8	593	9	AF145216
9	331	65.2	434	9	AF135381
10	318.5	62.7	495	6	AX079435
11	275	54.1	523	10	AF253064
12	245	48.2	207	6	AX330610
13	245	48.2	207	6	AX330787
14	245	48.2	207	6	AX331008
15	245	48.2	207	6	AX408097
16	238.5	46.9	682	10	AF253065
17	227.5	44.8	568	10	AY047360
18	215	42.3	151620	2	AC018589
19	215	42.3	180702	9	AC018557
20	215	42.3	188460	9	AC010542
21	142	28.0	97083	9	AC010289
22	139.5	27.5	527	10	AY046597
23	115	22.6	69937	2	AC121275
24	115	22.6	150552	2	AC121952
25	108	21.3	6283	6	AX252052
26	108	21.3	6283	6	AX344430
27	108	21.3	6283	6	AX344835
28	102	20.1	6283	6	AX252053
29	102	20.1	6283	6	AX344431
30	102	20.1	6283	6	AX344836
31	88	17.3	45416	9	AC000090
32	86.5	17.0	700	9	AF278577
33	86	16.9	159074	2	AC128918
34	85.5	16.8	13007	2	AE004148
35	83.5	16.4	792	14	AF105732
36	83.5	16.4	792	14	AF105741
37	83	16.3	37948	6	AF167558
38	82.5	16.2	508	10	AF401530
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40	81	15.9	627	14	AF094041
41	80.5	15.8	186873	2	AC115034
42	80.5	15.8	193819	2	AC116080
43	79.5	15.6	64425	9	AF1591368
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## ALIGNMENTS

RESULT 1

AX061624  
LOCUS AX061624 515 bp DNA linear PAT 24-JAN-2001  
DEFINITION Sequence 29 from Patent WO0100806.  
ACCESSION AX061624  
VERSION AX061624.1 GI:12406709  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 515)  
AUTHORS dumas mline Edwards,J.B., Bougueleret,L. and Jobert,S.  
TITLE Complementary dna's encoding proteins with signal peptides  
JOURNAL Patent: WO 0100806-A 29 04-JAN-2001;  
GENSET (FR)  
FEATURES  
source location/Qualifiers  
1..515  
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CDS  
144..443  
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144..287  
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Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
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Query Match: 100.00% Indels: 0  
Gaps: 0  
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DB 144 ATGATTAACGTGACACCGCAAAATAAACAATCCGCCCTTCTGCTTCACTGTAAGGACAC 203  
QY 21 ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40  
DB 204 GTGAAGATGCTCGCGCTGGATATATATCACTGTAACACAGTATTCATGCTCATC 263  
QY 41 ValSerValIleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
DB 264 GTATCTGTGTGGCACTGATACCAAGAACCAATGACAGTGGTGGAGGGGTCTT 323  
QY 61 AlaLeuValThrAlaValAlaCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80  
DB 324 GCACCTGTGTGACAGCAGTATGCTGTCTCCGACGGGCCCTTATTTACCGAAGCTTCTG 383  
QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99  
DB 384 TTCAATCCAGCGGTCTTACCAAGAAAGCCCTGTGATGAAAAAAGAGTTTGG 440

REFERENCE  
AUTHORS Han,W., Lou,Y., Tang,J., Zhang,Y., Chen,Y., Li,Y., Gu,W., Huang,J.,  
Gul,L., Tang,Y., Li,F., Song,Q., Di,C., Wang,L., Shi,Q., Sun,R.,  
Xia,D., Rui,M., Tang,J. and Ma,D.  
TITLE Molecular cloning and characterization of chemokine-like factor 1  
(CKLF1), a novel human cytokine with unique structure and potential  
chemotactic activity  
JOURNAL Biochem. J. 357 (Pt 1), 127-135 (2001)  
MEDLINE 21308461  
PUBMED 11415443  
REFERENCE  
2 (bases 1 to 530)  
AUTHORS Han,W.L., Li,Y., Zhang,Y.M., Di,C.H., Song,Q.S. and Ma,D.L.  
TITLE Direct Submission  
JOURNAL Submitted (03-OCT-1998) Immunology, Beijing Medical University, 38  
Xue Yuan Rd., Beijing 100083, China  
3 (bases 1 to 530)  
REFERENCE  
AUTHORS Han,W.L.  
TITLE Direct Submission  
JOURNAL Submitted (07-SEP-2000) Immunology, Peking University Health  
Science Center, Xueyuan Road 38, Beijing 100083, China  
REMARK  
COMMENT Sequence update by submitter  
FEATURES  
source On Sep 7, 2000 this sequence version replaced gi:6288733.  
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/db\_xref="taxon:9606"  
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/note="exposed to phytohaemagglutinin (PHA)"  
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/note="UCK-1"  
148..447  
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expression inhibited by IL-10"  
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/db\_xref="GI:6288734"  
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Alignment Scores:  
Pred. No.: 3 04e-56 Length: 530  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-09-801-115B-2 (1-99) x AF06895 (1-530)  
QY 1 MetaspasnaValGlnProLysIleLysHisArgProPheCysPheSerValIysGlyHis 20  
DB 148 ATGATTAACGTGACACCGCAAAATAAACAATCCGCCCTTCTGCTTCACTGTAAGGACAC 207  
QY 21 ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40  
DB 208 GTGAAGATGCTCGCGCTGGATATATCACTGTAACACAGTATTCATGCTCATC 267  
QY 41 ValSerValIleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
DB 268 GTATCTGTGTGGCACTGATACCAAGAACCAATGACAGTGGTGGAGGGGTCTT 327  
QY 61 AlaLeuValThrAlaValAlaCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80  
DB 328 GCACCTGTGACAGCAGTATGCTGTCTCCGACGGGCCCTTATTTACCGAAGCTTCTG 387  
QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99

Db 388 TTCATCCAGCGGCTCCTTACAGAAAGCCTGTGCATGAGAAAAAGAGTTTG 444

RESULT 3  
LOCUS AF057306 655 bp mRNA linear PRI 31-DEC-1999  
DEFINITION Homo sapiens transmembrane proteolipid (C32) mRNA, complete cds.  
ACCESSION AF057306  
VERSION AF057306.1 GI:6648618  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 655)  
Zhang, J.S., Nelson, M., Wang, L. and Smith D.I.  
Direct Submission  
Submitted (03-APR-1998) Pathology and Lab. Medicine, Mayo Clinic and Foundation, Rochester, MN 55905, USA  
FEATURES  
source location/Qualifiers  
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/cell\_line="ASPC-1"  
/tissue\_type="pancreas"  
/note="adenocarcinoma"  
1..655  
/gene="C32"  
132..590  
/gene="C32"  
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BASE COUNT 171 a 137 c 153 g 194 t

ORIGIN

Alignment Scores:  
Pred. No.: 1,99e-51 Length: 655  
Score: 471.50 Matches: 99  
Percent Similarity: 65.13% Conservative: 0  
Best Local Similarity: 65.13% Mismatches: 0  
Query Match: 92.81% Indels: 53  
DB: 9 Gaps: 1

US-09-801-115B-2 (1-99) x AF057306 (1-655)

QY 1 MetaspasvAlGInProLysIleLysHISArpProPhesCysPheSerValLysGLYHis 20  
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Db 132 ATGGATTAACGTGCAGCGCGAATAAATACATCGCCCTTCTCTCAAGTGTGAAGGCCAC 191

QY 21 VallysMetLeuArg----- 25  
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Db 192 GTGAAGATGCTGGCGCTGGCACTAAGTGAACGTATGACCTTTTATCATGCACAA 251

QY 25 ----- 25

Db 252 GCCCCTGAACATATATTGTTATCATCGATTGGAAGTGAACCGTTATCTATTTCATA 311

QY 26 -----LeuAsp 27  
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Db 312 CTTTATATATGACTAGACTGATGATTAATGAAGTGGTATTGTCCTTTGCTTGAT 371

QY 28 IleIleasnSerLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle 47  
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Db 372 ATTATCAACTCACTGCTGAACAACAGTATTCATGCTCATGCTATGCTGTGGCACTGATA 431

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Db 432 CCAGAAACCAACAATTCAGACTGTGTGGAGGGGTGTTTGCATTGTGACACGACTATGC 491

QY 68 CysLeuAlaAspGlyValAlaLeuIleTyrArgLysIleLeuPheAsnProSerGlyProTyr 87  
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Db 492 TGTCTGGCCGACGGGGCCCTTATTTACCGGAAGCTTGTTCAATCCACAGCGGCTTAC 551

QY 88 GlnLysLysProValHisGlnLysLysGluValLeu 99  
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Db 552 CAGAAAGACCTGTGCATGAGAAAAAGAGTTTG 587

RESULT 4  
LOCUS AX061665 669 bp DNA linear PAT 24-JAN-2001  
DEFINITION Sequence 70 from Patent WO0100806.  
ACCESSION AX061665  
VERSION AX061665.1 GI:12406789  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 669)  
dumas Milne Edwards, J.B., Bouquelieret, L. and Jobert, S.  
Complementary dna's encoding proteins with signal peptides  
Patent: WO 0100806-A 70 04-JAN-2001;  
GENSET (FR)  
FEATURES  
source location/Qualifiers  
1..669  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
140..598  
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/db\_xref="GI:12406790"  
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YIVTGEVAVILFFILLYLRDLRMLKWLFWPLDILNSIVTFVFMILVSLALPE  
TTTLVGGGVAVLTAVCCIALDGLIYRLKILNPSGPYQKPKVHEKREV"  
140..442  
/note="Von Heijne matrix score 4.10 seq VFMILVSLALPE/ET"  
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polyA\_signal  
polyA\_site 630..635  
BASE COUNT 178 a 139 c 158 g 194 t

ORIGIN

Alignment Scores:  
Pred. No.: 2,04e-51 Length: 669  
Score: 471.50 Matches: 99  
Percent Similarity: 65.13% Conservative: 0  
Best Local Similarity: 65.13% Mismatches: 0  
Query Match: 92.81% Indels: 53  
DB: 6 Gaps: 1

US-09-801-115B-2 (1-99) x AX061665 (1-669)

QY 1 MetaspasvAlGInProLysIleLysHISArpProPhesCysPheSerValLysGLYHis 20  
|||||

Db 140 ATGGATTAACGTGCAGCGCGAATAAATACATCGCCCTTCTCTCAAGTGTGAAGGCCAC 199

QY 21 VallysMetLeuArg----- 25  
|||||

Db 200 GTGAAGATGCTGGCGCTGGCACTAAGTGAACGTATGACCTTTTATCATGCACAA 259

QY 25 ----- 25

Db 260 GCCCCTGAACATATATTGTTATCATCGATTGGAAGTGAACCGTTATCTATTTCATA 319

QY 26 -----LeuAsp 27  
|||||

Db 320 CTTTATATATGACTAGACTGATGATTAATGAAGTGGTATTGTCCTTTGCTTGAT 379

QY 28 IleIleasnSerLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle 47  
|||||

[illegible]

ORIGIN	Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:
US-09-801-115B-2 (1-99) x BC004380 (1-688)	2,11e-51	Length: 688	471.50	65.13%	Matches: 99	
					Conservative: 0	
					Mismatches: 0	
					Indels: 53	
		Gaps: 1				
QY	1	MetaSpasVaIGInProLySileYsHsArGProPhSeCySPhSeSerValLySgLYHs	20			
Db	137	ATGGAATACGTCGACGCGAAATATAAAGTTCGCCCTTCTGCTTCAAGTGTGAAGGCCAC	196			
QY	21	ValLySMeLleuArg-----	25			
Db	197	GTAAGATGCTCGCGCTGCGACTAAGTGCATCTATGACCTTTTATCATCGCACAA	256			
QY	25	-----	25			
Db	257	GCCTCGAACCATATATTGTTATCATCTGGAATTTGAAGTACCCCTTATCTATTTTCATA	316			
QY	26	-----Leuasp	27			
Db	317	CTTTATATGACCTGACACTGATGATTAATGAAGTGGTTATTTTGGCTTTGGCTTGAT	376			
QY	28	IlelleaSenSerLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle	47			
Db	377	ATTATCAACTCATCTGTGTAACAACACATATTCAATGCAATCGATATCTGTGTGGCACTGATA	436			
QY	48	ProGluThrThrThrLeuThrValGlyGlyValAlaPheAlaLeuValThrAlaValCys	67			
Db	437	CCAGAAACACACAATGTACAGTTGTGTGGAGGGGTGTTGCACCTGTGACAGCACTATAC	496			
QY	68	CysLeuAlaAPGlyAlaLeuIleIleYrArgLySLeuLeuPheAsnProSerGlyProTyr	87			
Db	497	TGCTGTCCGACGGGGCCCTTATTTAACGGAAGCTTCTGTTCAATCCAGGGCTCTTAC	556			
QY	88	GlnLySLysProValIHisGluLySLysGluValLeu	99			
Db	557	CAGAAAAAGCCTGTGTCATGAAAAAAGAAAGATTGG	592			
RESULT 6	AF135380	689 bp	mRNA	linear	PRI 07-SEP-2000	
LOCUS	AF135380					
DEFINITION						
ACCESSION						
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
REMARK						
COMMENT						
FEATURES						
source						

gene /note="from PHA stimulated cells"  
1.689  
/gene="CKIF2"  
/note="UCK"  
148.606  
CDS /gene="CKIF2"  
/note="UCK-2; alternatively spliced"  
/codon\_start=1  
/product="chemokine-like factor 2"  
/protein\_id="AF19599.1"  
/db\_xref="GI:6630854"  
/translation="MDNVQPKIKRPFCSVKGVMMLALTVSMPTFIQAPEP  
YIVTGEVTVILFLLVLRDLKMLFPLDINSIVTFMLIVSLALPE  
TTTTLVGGGVFALVTAVCCADGALYIRKLFPSPGYOKRKEVEVL"

BASE COUNT 195 a 140 c 161 g 193 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2.11e-51 Length: 689  
Score: 471.50 Matches: 99  
Percent Similarity: 65.13% Conservative: 0  
Best Local Similarity: 65.13% Mismatches: 0  
Query Match: 92.81% Indels: 53  
DB: 9 Gaps: 1

US-09-801-115B-2 (1-99) x AF135380 (1-689)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIysGlyHis 20  
DB 148 ATGATACGATGCTGACGCCGAAATTAACATCGCCCTCGCTTCAGTGTGAAGGCCAC 207  
QY 21 ValIysMetLeuArg----- 25  
DB 208 GTGAAGATGCTGGCGTGGCACTAGTGCATATGACCTTTTATCATCGACAA 267  
QY 25 ----- 25  
DB 268 GCCCGTGAACCATATATTGTATACACTGGATTTGAAGTACCGTATCTATTTCATCA 327  
QY 26 -----LeuAsp 27  
DB 328 CTTTATATGACTGACACTGATGATGATTAATGACGTTGTTTGGCTTGTGAT 387  
QY 28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValIleuAlaLeuIle 47  
DB 388 ATATCACTGATGCTGATCAACACATTCATGCTCATGCTGATCTGTGGCAGTATA 447  
QY 48 ProGluThrThrThrLeuThrValGlyGlyGlyValPheAlaLeuValThrAlaValCys 67  
DB 448 CCGAAGAACCAACATGACAGTGTGGAGGGGTGTTGCACTTGTGACAGCAGTATGC 507  
QY 68 CysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSerGlyProTyr 87  
DB 508 TGCTCTGCCGACGGGGCCCTTATTACCGGAAGCTTCTGTCAATCCAGCGGTCTTAC 567  
QY 88 GlnLysLysProValHisGlnLysLysGluValLeu 99  
DB 568 CAGAAAAAGCCTGTGCATGAAAAAAGAGTTTTC 603

RESULT 7  
G30204 485 bp DNA linear STS 05-OCT-1996  
LOCUS human STS SHGC-36487, sequence tagged site.  
ACCESSION G30204  
VERSION G30204.1 GI:1593755  
KEYWORDS STS; STS sequence; primer; sequence tagged site.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 485)  
AUTHORS Myers,R.M.  
JOURNAL Unpublished (1996)

COMMENT

Contact: Richard M. Myers  
Stanford Human Genome Center (SHGC)  
Stanford University School of Medicine  
Department of Genetics, M-344, Stanford, CA 94305, USA  
Tel: 4157259687  
Fax: 4157259689  
Email: myers@shgc.stanford.edu

Primer A: ACCTCTTTTTCATGACAGG  
Primer B: GCCCTTATTACCGAAGCT  
STS size: 77  
PCR Profile:  
Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds  
Annealing: 62 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9600  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Tag Polymerase: 0.05 units/uL  
Total Vol: 10 uL

Buffer: MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from T90565  
-- Washington University/Merk EST sequence.

FEATURES  
source 1..485  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/map="16"

STS  
primer\_bind 69..91  
primer\_bind complement(126..145)  
BASE COUNT 146 a 99 c 99 g 131 t 10 others  
ORIGIN

Alignment Scores:  
Pred. No.: 5.4e-38 Length: 485  
Score: 366.00 Matches: 73  
Percent Similarity: 98.65% Conservative: 0  
Best Local Similarity: 98.65% Mismatches: 1  
Query Match: 72.05% Indels: 0  
DB: 11 Gaps: 0

US-09-801-115B-2 (1-99) x G30204 (1-485)

QY 26 LeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValIleuAla 45  
DB 286 CTTGATATTATCACTGCTGATCAACACATTCATGCTCATGCTGATCTGTGGCA 227  
QY 46 LeuIleProGluThrThrThrLeuThrValGlyGlyGlyValPheAlaLeuValThrAla 65  
DB 226 CTGATACGAAACCAACATTCAGCTGTGGAGGGGTGTTGCACTTGTACAGCA 167  
QY 66 ValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSerGly 85  
DB 166 GTATGCTGCTTGGCGACGGGGCCCTTATTACCGGAAGCTTCTGTCAATCCAGGGGT 107  
QY 86 ProTyrGlnLysLysProValHisGlnLysLysGluValLeu 99  
DB 106 CCTTACCGAAAAAGCCTGTGCATGAAAAAAGAGTTTTC 65  
RESULT 8

Db	370	TTTTGGCGCTTGGCTTGTGTTGGCACTTGTGACACAGATAGCTGTCTTGGCGAGGGGCC	429
Oy	74	LeuiletyrA-glyLeuLeuPheAsnProSerGlyProTyrGlnIlySLysProValHis	93
Db	430	CTTATTTTACCGGAGAGCTTGTGTTCAATCCAGCGGCTTACACGAAAAAGCCGTGCAT	489
Oy	94	GIuIySLysGIuValIeu 99	
Db	490	GAATAAAGAGAGTTTGG 507	
RESULT 9			
LOCUS	AF135381	434 bp	mRNA
DEFINITION	Homo sapiens chemokine-like factor 3 (CKLF3) mRNA, complete cds,		
ACCESSION	AF135381		
VERSION	AF135381.2		
KEYWORDS	GI:9989693		
SOURCE			
ORGANISM	Homo sapiens.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 434)		
TITLE	Han,W.L., Gu,W., Li,Y., Zhang,Y., Song,Q., Di,C. and Ma,D.		
JOURNAL	Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue		
REFERENCE	Yuen Road, Beijing 100083, China		
AUTHORS	2 (bases 1 to 434)		
TITLE	Han,W.L.		
JOURNAL	Direct Submission		
REMARK	Submitted (07-SEP-2000) Immunology, Peking University Health		
COMMENT	Science Center, Xueyuan Road 38, Beijing 100083, China		
FEATURES	Sequence update by submitter		
SOURCE	On Sep 7, 2000 this sequence version replaced gi.6630855.		
	Location/Qualifiers		
	1. 434		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/cell_line="0937"		
	/note="from PHA stimulated cells"		
	1. .434		
	/gene="CKLF3"		
	/note="vJuck"		
	148. .351		
	/gene="CKLF3"		
	/note="vJuck-3; alternatively spliced"		
	/codon_start=1		
	/product="chemokine-like factor 3"		
	/protein_id="AAFI9600.1"		
	/db_xref="GI:6630856"		
	/translation="MDNVQPIKIRPCEFSYKGVHKMLRLVFLVTVAVCLADGALTY		
	RKLLFNPSGPOKKPVEKKEVLT"		
BASE COUNT	127 a 88 c 116 g 103 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	1.52e-33	Length:	434
Score:	331.00	Matches:	67
Percent Similarity:	67.68%	Conservative:	0
Best local Similarity:	67.68%	Mismatches:	0
Query Match:	65.16%	Indels:	32
DB:	9	Gaps:	1
US-09-801-115B-2	x AF135381 (1-434)		
Oy	1	MetaspasnaValGlnProIySLyIleLyHisArGProPheCySPheSerValIySGlyHis	20
Db	148	ATGATATACGTCGACGCGGAAATAAACATCGGCCCTTCGTGCTCAGTGGAAGGCAC	207
Oy	21	ValIySmetLeuAArgLeuAspIleIleAsnSerIeuValIhrThrValPmetLeuIle	40
Db	208	GTGAAGATGTCGCGGCTG-----	225



QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
 Db 226 -----GTGTTT 231  
 QY 61 AlaLeuValThrAlaValAlaCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80  
 Db 232 GCACCTGTGACAGAGTATGCTGCTCCGACGGGGCCCTTATTACCGGAGCTCTG 291  
 QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99  
 Db 292 TTCATTCACGCGGCTCTTACCAGAAAGCCTGTGATGAAAGAGAGAGTTTG 348  
 RESULT 10  
 AX079435 495 bp DNA linear PAT 22-FEB-2001  
 LOCUS Sequence 179 from Patent WO0107611.  
 DEFINITION AX079435  
 ACCESSION AX079435 GI:13158995  
 VERSION AX079435.1 GI:13158995  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 1 (bases 1 to 495)  
 AUTHORS Baker, K.P., Goddard, A. and Wood, W.I.  
 TITLE Human polypeptides and methods for the use thereof  
 JOURNAL Patent: WO 0107611-A 179 01-FEB-2001;  
 Genentech, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
 1..495  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 119 a 103 c 127 g 142 t 4 others  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 7.3e-32 Length: 495  
 Score: 318.50 Matches: 70  
 Percent Similarity: 56.45% Conservative: 0  
 Best Local Similarity: 56.45% Mismatches: 1  
 Query Match: 62.70% Indels: 53  
 DB: 6 Gaps: 1  
 US-09-801-115b-2 (1-99) x AX079435 (1-495)  
 QY 1 MetAspAsnValAlaGlnProLysIleLeuHisArgProPhcysPheSerValLysGlyHis 20  
 Db 124 ATGGATTAACGTGACGCGGAAATAAATCAATCGCCCTCTGCTCAAGTGAAGGCGAC 183  
 QY 21 ValLysMetLeuArg----- 25  
 Db 184 GTGAAGATCTGCGGCTGCGCACTAACTGACATCTATGACCTTTTATATATATCGACAA 243  
 QY 25 ----- 25  
 Db 244 GCCCCTGACATATATATGTATCACTGATTTGAAGTCACCGCTATCTATTATTTCAATA 303  
 QY 26 -----LeuAsp 27  
 Db 304 CTTTATATAGTACTGAGACTGATGATTAATGAAGTGTATTTTGGCCCTTGCTTGTAT 363  
 QY 28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle 47  
 Db 364 ATTATCACTCACTGATGATTAACACAGATTCATGCTATCTGTGTGGCAGCTGATA 423  
 QY 48 ProGluThrThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValLys 67  
 Db 424 CCAGAAACCAACAACATTGACAGTGTGGTGGAGGGGTGTTGCACTGTTGACACAGATATGC 483  
 QY 68 CysLeuAlaAsp 71  
 Db 484 TGTNTTGGCGAC 495

RESULT 11  
 AF253064 523 bp mRNA linear ROD 27-NOV-2001  
 LOCUS Rattus norvegicus chemokine-like factor 1 (Ck1f1) mRNA, complete  
 DEFINITION  
 ACCESSION AF253064  
 VERSION AF253064.2 GI:17105378  
 KEYWORDS  
 SOURCE  
 ORGANISM Rattus norvegicus.  
 Rattus norvegicus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 523)  
 Lou, Y., Li, Y., Han, W., Song, Q., Zhang, Y., Di, C. and Ma, D.  
 Direct Submission  
 Submitted (06-APR-2000) Immunology, Beijing Medical University,  
 Xueyuan Road, Beijing 100083, China  
 2 (bases 1 to 523)  
 Lou, Y., Li, Y., Han, W., Song, Q., Zhang, Y., Di, C. and Ma, D.  
 Direct Submission  
 Submitted (27-NOV-2001) Immunology, Beijing Medical University,  
 Xueyuan Road, Beijing 100083, China  
 Sequence update by submitter  
 On Nov 27, 2001 this sequence version replaced gi:7769680.  
 REMARK  
 COMMENT  
 FEATURES  
 source Location/Qualifiers  
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 /organism="Rattus norvegicus"  
 /strain="Wistar"  
 /db\_xref="taxon:10116"  
 /tissue\_type="liver"  
 1..523  
 /gene="Ck1f1"  
 167..463  
 /note="Ck1f1"  
 /note="cytokine; similar to Homo sapiens Ck1f1"  
 /product="chemokine-like factor 1"  
 /protein\_id="AA069502.1"  
 /db\_xref="GI:7769681"  
 /translation="WDSPQKVDHQPCLSLKCFVTKLRLDVINSVVTLLFMILYSV  
 ALPEISTMTIMVGFGFLTYICVADCALMCKLRPRRPGPPQNSADVDVS"  
 BASE COUNT 134 a 107 c 133 g 149 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.14e-26 Length: 523  
 Score: 275.00 Matches: 53  
 Percent Similarity: 76.67% Conservative: 16  
 Best Local Similarity: 58.89% Mismatches: 21  
 Query Match: 54.13% Indels: 0  
 DB: 10 Gaps: 0  
 US-09-801-115b-2 (1-99) x AF253064 (1-523)  
 QY 1 MetAspAsnValAlaGlnProLysIleLeuHisArgProPhcysPheSerValLysGlyHis 20  
 Db 167 ATGACATCTCCACAGAGAGTGTAGACCATCAGCCCTTGCCCACTCGAATGCTTT 226  
 QY 21 ValLysMetLeuArgLysLeuAlaLeuIleAsnSerLeuValThrThrValPheMetLeuIle 40  
 Db 227 GTGAAGACGCTGCGGTTGGATGATATCACTGCGTGAACACATATTCATGCTTAT 286  
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
 Db 287 GTGCTGTGCTGCTGCTATATACCAAGAAACCAACATGATGAAGTGGAGGGGTGTT 346  
 QY 61 AlaLeuValThrAlaValAlaCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80  
 Db 347 GGTTCCTGACAGATATATGATGCTGCTGCTATGTCCTTATGTCGCAAGAACTCGCG 406  
 QY 81 PheAsnProSerGlyProTyrGlnLysLys 90

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Db      407 TTTCGTCCACATGACCTTATCAGAACAG 436
RESULT 12
AX330610/c      207 bp      DNA      linear      PAT 09-JAN-2002
LOCUS      AX330610
DEFINITION      Sequence 1119 from Patent WO0194629.
ACCESSION      AX330610
VERSION      AX330610.1 GI:18103588
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE      1
AUTHORS      Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE      Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL      Patent: WO 0194629-A 1119 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source      1..207
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT      70 a      43 c      39 g      54 t      1 others
ORIGIN
Alignment Scores:
Pred. No.:      7,42e-23      Length:      207
Score:      245.00      Matches:      47
Percent Similarity:      97.92%      Conservative:      0
Best Local Similarity:      97.92%      Mismatches:      1
Query Match:      48.23%      Indels:      0
Gaps:      0
US-09-801-115b-2 (1-99) x AX330610 (1-207)
QY      52 ThrleuThrValGlyGlyGlyValPheAlaLeuValThraAlaValCysCysLeuAlaasp 71
|||||
Db      205 ACATTGACAGTTGGTGGAGGGGCTTTCACCTTGACACGACGATGCTGCTTCCGCAC 146
|||||
QY      72 GlyAlaLeuIleTyArgLysLeuPheAsnProSerGlyProTyGlnLysLysPro 91
|||||
Db      145 GGGGCCCTTATTACCGGAGGCTCTGTCATCCACGCGCTTACACGNAAGGCT 86
|||||
QY      92 ValHisGlnLysLysGlnValLeu 99
|||||
Db      85 GTGCATGAAAAAAGAGATTGG 62
|||||
RESULT 13
AX330787/c      207 bp      DNA      linear      PAT 09-JAN-2002
LOCUS      AX330787
DEFINITION      Sequence 1296 from Patent WO0194629.
ACCESSION      AX330787
VERSION      AX330787.1 GI:18103765
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE      1
AUTHORS      Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE      Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL      Patent: WO 0194629-A 1296 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source      1..207
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT      70 a      43 c      39 g      54 t      1 others

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ORIGIN
Alignment Scores:
Pred. No.:      7,42e-23      Length:      207
Score:      245.00      Matches:      47
Percent Similarity:      97.92%      Conservative:      0
Best Local Similarity:      97.92%      Mismatches:      1
Query Match:      48.23%      Indels:      0
Gaps:      0
US-09-801-115b-2 (1-99) x AX330787 (1-207)
QY      52 ThrleuThrValGlyGlyGlyValPheAlaLeuValThraAlaValCysCysLeuAlaasp 71
|||||
Db      205 ACATTGACAGTTGGTGGAGGGGCTTTCACCTTGACACGACGATGCTGCTTCCGCAC 146
|||||
QY      72 GlyAlaLeuIleTyArgLysLeuPheAsnProSerGlyProTyGlnLysLysPro 91
|||||
Db      145 GGGGCCCTTATTACCGGAGGCTCTGTCATCCACGCGCTTACACGNAAGGCT 86
|||||
QY      92 ValHisGlnLysLysGlnValLeu 99
|||||
Db      85 GTGCATGAAAAAAGAGATTGG 62
|||||
RESULT 14
AX331008/c      207 bp      DNA      linear      PAT 09-JAN-2002
LOCUS      AX331008
DEFINITION      Sequence 1517 from Patent WO0194629.
ACCESSION      AX331008
VERSION      AX331008.1 GI:18121642
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE      1
AUTHORS      Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE      Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL      Patent: WO 0194629-A 1517 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source      1..207
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT      70 a      43 c      39 g      54 t      1 others
ORIGIN
Alignment Scores:
Pred. No.:      7,42e-23      Length:      207
Score:      245.00      Matches:      47
Percent Similarity:      97.92%      Conservative:      0
Best Local Similarity:      97.92%      Mismatches:      1
Query Match:      48.23%      Indels:      0
Gaps:      0
US-09-801-115b-2 (1-99) x AX331008 (1-207)
QY      52 ThrleuThrValGlyGlyGlyValPheAlaLeuValThraAlaValCysCysLeuAlaasp 71
|||||
Db      205 ACATTGACAGTTGGTGGAGGGGCTTTCACCTTGACACGACGATGCTGCTTCCGCAC 146
|||||
QY      72 GlyAlaLeuIleTyArgLysLeuPheAsnProSerGlyProTyGlnLysLysPro 91
|||||
Db      145 GGGGCCCTTATTACCGGAGGCTCTGTCATCCACGCGCTTACACGNAAGGCT 86
|||||
QY      92 ValHisGlnLysLysGlnValLeu 99
|||||
Db      85 GTGCATGAAAAAAGAGATTGG 62
|||||
RESULT 15
AX408097/c

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LOCUS AX408097 207 bp DNA linear PAT 14-JUN-2002  
 DEFINITION Sequence 744 from Patent WO229103.  
 ACCESSION AX408097  
 VERSION AX408097.1 GI:21440802  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS 1  
 TITLE Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.  
 JOURNAL Gene expression profiles in liver cancer  
 Patent: WO 0229103-A 744 11-APR-2002;  
 GENE LOGIC INC (US)  
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